

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2006, 10:42:19 ; Search time 949 Seconds
(without alignments)
10195.124 Million cell updates/sec

Title: US-10-626-398-7
Perfect score: 1170
Sequence: 1 atgttggaataaacagtagc.....accgtcaatataccacttga 1170

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	1170	8	US-10-626-445-7
2	1170	100.0	1170	9	US-10-626-126-7
3	1170	100.0	1170	9	US-10-626-398-7
4	675	57.7	1170	9	US-10-488-421-7
5	675	57.7	1173	3	US-09-812-216-1
6	675	57.7	1173	3	US-09-910-411-1
7	675	57.7	1173	3	US-09-875-076-13
8	675	57.7	1173	3	US-09-876-252-13
9	675	57.7	1173	5	US-10-052-193-1
10	675	57.7	1173	6	US-10-272-983-13
11	675	57.7	1173	6	US-10-354-769-1
12	675	57.7	1173	6	US-10-393-807-13
13	675	57.7	1173	6	US-10-417-820A-13
14	675	57.7	1173	7	US-10-349-253A-1
15	675	57.7	1173	7	US-10-723-955-13
16	675	57.7	1173	7	US-10-782-596-13
17	675	57.7	1173	7	US-10-737-619-1
18	675	57.7	1173	8	US-10-626-445-1
19	675	57.7	1173	9	US-10-616-088-1
20	675	57.7	1173	9	US-10-626-126-1
21	675	57.7	1173	9	US-10-626-398-1
22	675	57.7	1173	9	US-10-723-955-13
23	675	57.7	1266	3	US-09-891-138A-5

ALIGNMENTS

RESULT 1

US-10-626-445-7
; Sequence 7, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-445-7

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Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy	1	ATGTTGGCAATAACAGTCAATCGGCTTAACATCAATTAATAATTTCTTTGACATTTTAA 60		
Db	1	ATGTTGGCAATAACAGTCAATCGGCTTAACATCAATTAATAATTTCTTTGACATTTTAA 60		
Qy	61	ATGCTTTTACTAGCTATTCCTAATGTTAGGCAATGTCGTGTCATTTTATGCTTTTATT 120		
Db	61	ATGCTTTTACTAGCTATTCCTAATGTTAGGCAATGTCGTGTCATTTTATGCTTTTATT 120		
Qy	121	GTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTTGGCCATTCGACAC 180		
Db	121	GTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTTGGCCATTCGACAC 180		
Qy	181	TTCTTTTGGGTGCAATTCCTCTGTATCATCTTCCTCGCTGACTTACTGACT 240		
Db	181	TTCTTTTGGGTGCAATTCCTCTGTATCATCTTCCTCGCTGACTTACTGACT 240		
Qy	241	TCTGGGAAGCAAGCTTGTGTAATTTTGGCTCATTTACTGACTATCTTTTATGACGACTCT 300		
Db	241	TCTGGGAAGCAAGCTTGTGTAATTTTGGCTCATTTACTGACTATCTTTTATGACGACTCT 300		

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301 GTGTATAATATTGTCCTCATCAGCTACGATCGCTACCAAGTCAGTCTCAATGCGGTGG 360
Db GTGTATAATATTGTCCTCATCAGCTACGATCGCTACCAAGTCAGTCTCAATGCGGTGG 360
361 TATAGAGCTCAGCACTCTGGCACCCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420
Db TATAGAGCTCAGCACTCTGGCACCCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420
421 TTCTCTTCAATGCAAAATGGGCGGATGATTCGATTTAGCTCTTGGCAGAAATAGCACT 480
Db TTCTCTTCAATGCAAAATGGGCGGATGATTCGATTTAGCTCTTGGCAGAAATAGCACT 480
481 ACAGAAATGCAACTGGAATTTTAAAGAGTGTGTTCTCTCTCTCTCTCTCTCTCTCTCT 540
Db ACAGAAATGCAACTGGAATTTTAAAGAGTGTGTTCTCTCTCTCTCTCTCTCTCTCTCT 540
541 GAATTCCTGATCCCATCTTTGTTAGTTGCTTATTTAGCGCCCATATTTTCTGAGCCCTG 600
Db GAATTCCTGATCCCATCTTTGTTAGTTGCTTATTTAGCGCCCATATTTTCTGAGCCCTG 600
601 TGAAGCGGAGAGAACTGAGCAGGTGCTCAGCAAGCTGCTCTCTCTCTCTCTCTCTCTCT 660
Db TGAAGCGGAGAGAACTGAGCAGGTGCTCAGCAAGCTGCTCTCTCTCTCTCTCTCTCTCT 660
661 AGCAGTGACCAAGCAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGCTCTGCCAGCA 720
Db AGCAGTGACCAAGCAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGCTCTGCCAGCA 720
721 CGAAAGAAACAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db CGAAAGAAACAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
781 TTTTCCATAGAGCCTACAAGAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCTCC 840
Db TTTTCCATAGAGCCTACAAGAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCTCC 840
841 CACTCAGATTCCTGGCTCTTCAAGAAAGGAAACATATCGAACTTTTTCAGAGCCAGAAA 900
Db CACTCAGATTCCTGGCTCTTCAAGAAAGGAAACATATCGAACTTTTTCAGAGCCAGAAA 900
901 TTAGCCAAAGTCACTGGCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATCA 960
Db TTAGCCAAAGTCACTGGCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATCA 960
961 CTGACTACAGTTATCTACTCAATTTTCTGAAAGGAACTTGACTAAATCAACTGGTAC 1020
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1021 CATACTGCTTTTGGCTCCAGTGGTTCAATTCCTTTGTTAATCCCTTTTGTATCCATTG 1080
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Db CCACCAACAAACCGCTCAATATCCACTTGA 1170
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RESULT 2
US-10-626-126-7
; Sequence 7, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCES: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23

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; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
; US-10-626-126-7  
  
Query Match 100.0%; Score 1170; DB 9; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 ATGTTGGCAAAATTAACAGTACAATCGCTTTAAACATCAATCAATTAATTTCTTTGACATTTTA 60  
61 ATGTCCTTTACTAGCTAATGCTATAATGTTAGGCAATGTCGTGTCATTTTAGCTTTTATT 120  
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Db 121 GTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCCATTGCAGAC 180  
181 TTCTTTGCGGTGCAATGCAATTCCTCTGTATACATACCTTCTCGCTGACTTAATCTGGACT 240  
Db 181 TTCTTTGCGGTGCAATGCAATTCCTCTGTATACATACCTTCTCGCTGACTTAATCTGGACT 240  
241 TCTGGAAAGCAAGCTTGTGTATTTTGGCTCAATTAATCTTTTATGTACAGCATCT 300  
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301 GTGTATAATATTGTCCTCATCAGCTACGATCGCTACAGTCAGTCTCAAAATGCGGTGG 360  
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361 TATAGAGCTCAGCACTCTGGCACCCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420  
Db 361 TATAGAGCTCAGCACTCTGGCACCCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420  
421 TTCTCTCTTCAATGCAAAATGGGCGGATGATTCGATTTAGCTCTTGGCAGAAATAGCACT 480  
Db 421 TTCTCTCTTCAATGCAAAATGGGCGGATGATTCGATTTAGCTCTTGGCAGAAATAGCACT 480  
481 ACAGAAATGCAACTGGAATTTTAAAGAGTGTGTTCTCTCTCTCTCTCTCTCTCTCTCT 540  
Db 481 ACAGAAATGCAACTGGAATTTTAAAGAGTGTGTTCTCTCTCTCTCTCTCTCTCTCTCT 540  
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Db 661 AGCAGTGACCAAGCAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGCTCTGCCAGCA 720  
721 CGAAAGAAACAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
Db 721 CGAAAGAAACAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
781 TTTTCCATAGAGCCTACAAGAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCTCC 840  
Db 781 TTTTCCATAGAGCCTACAAGAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCTCC 840  
841 CACTCAGATTCCTGGCTCTTCAAGAAAGGAAACATATCGAACTTTTTCAGAGCCAGAAA 900
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; PRIOR APPLICATION NUMBER: US 60/332,697
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent
; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.
; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequence
; OTHER INFORMATION: only
; NAME/KEY: misc feature
; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462
; OTHER INFORMATION: are AAG and 988 is C
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; US-10-488-421-7
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; Query Match 57.7%; Score 675; DB 9; Length 1170;
; Best Local Similarity 74.9%; Pred. No. 7.5e-185;
; Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
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Query Match 57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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Db 71 TAGTAGCTTTTGTCTATTAATGTTAGGCAATGTCGTCATTTTAACTTTTAAATGTCCT 130

Qy 128 GAATCTTTAGCATCGAATGTTACTTTTCTTAACCTTGGCCATTCGACATTCCTTTG 187
Db 131 AAAACCTTTAGCATCGAATGTTACTTTTCTTAACCTTGGCCATTCGACATTCCTTTG 190

Qy 188 TGGGTGCAATGCAATTCCTGTACATACCTTCTGCTGCTGCTTACTTGGACTTCTGAA 247
Db 191 TGGGTGCAATGCAATTCCTGTACATACCTTCTGCTGCTGCTTACTTGGACTTCTGAA 250

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Db 251 AGCAAGCTTGTGATTTTGGCTCATTTACTGACTATCTTTTATGATGACATCTCTGTATA 310

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Qy 368 CTCAGCACTCTGGCACCCTGGAAATTCCTACTAGTGGGCTGTTGGATATTCCTCT 427
Db 371 CTCAGCACTCTGGGCTTGGAAATTCCTACTAGTGGGCTGTTGGATATTCCTCTCT 430

Qy 428 TCATGACAAATGGGCGCATGATTCGATTTTCAAGTCTTGGCAGATAGCACTACAGAT 487
Db 431 TCTTAGTGAATGGGCGCATGATTCGATTTTCAAGTCTTGGCAGATAGCACTACAGAT 490

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Db 491 GTGAACCTGGATTTTAAAGTGGTACTTTGCTCTCCCTACATCATATTAGGAATTC 550

Qy 548 TGATCCCATCTGTTAGTTCCTTATTTTCAAGGCGCCATATTTTCTGAGGCTGTTGGAGC 607
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Qy 608 GAGAGAACTCAGCAGAGTGCCTCAGCCACCTGCTGCTCTCCCTCTGACTCTTCCAGCAGTG 667
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Qy 668 ACCAGGACACTCTGTCAGACAGGACCCCGATTCAGGGGCGACTCTGCCAGACGGAAAG 727
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Db 728 AAGTCTCTGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 787

Qy 788 TAAGAGCTCAAGAACAGCAATGTGATCGCTTCCAAATGCGCTCTCTCCCACTCAG 847
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Db 908 AGTCACTGGCCATCTCTTAGCAGCTTTTGGCATTTTGGCTTGGCTTGGCTTGGCTTGGCT 967

Qy 968 CAGTTATCTACTCATTTTCTGAAAGGAACTTGGATCAATCAACCTGTTGATCATACTG 1027
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RESULT 6

US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergema, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AKOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match 57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATAACAGTACCAATCGCCTTAACATCAATTAATAAATCTTTGACATTTTAAATGTCCT 67
Db 11 CTAATAGCACATCAATTTATACATAGCACTCGTGTACTTTAGCATTTTATGTCCT 70

Qy 68 TACTAGCTATTGCTATTAATGTTAGGCAATGTCGTCATTTTAACTTTTAAATGTCCT 127
Db 71 TAGTAGCTTTTGTCTATTAATGTTAGGCAATGTCGTCATTTTAACTTTTAAATGTCCT 130

Qy 128 GAATCTTTAGCATCGAATGTTACTTTTCTTAACCTTGGCCATTCGACATTCCTTTG 187
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Qy 188 TGGGTGCAATGCAATTCCTGTACATACCTTCTGCTGCTGCTTACTTGGACTTCTGAA 247
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Qy 308 ATATTGCTCTCATGAGTACGATCGCTACAGTCACTTCAATGCGGTGTTAGATAGAG 367
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Qy 368 CTCAGCACTCTGGCACCCTGGAAATTCCTACTAGTGGGCTGTTGGATATTCCTCT 427
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Qy 428 TCATGACAAATGGCCGATGATTCGATTTTCAGACTCTTGGCAGAAATAGCACTACAGAT 487
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Db 491 GTGAACCTGGATTTTTCGGATGGTACATCCTTGGCATCACATCATCTTGGAAATCG 550
Qy 548 TGATCCCACTCTGTTAGTGTCTTATTTTCAGCGCCCATATTTACTGAGCGCTGGGAAC 607
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Db 611 GTGATCATCTCAGTAGTGCCAAAGCCATCTGACTGATGCTGTCTCTTCCACAA--- 667
Qy 668 ACCACGACACTCTGTCAGACAGGACCCGATTCAGGGCGACTCTGCCAGCAGCGAAAG 727
Db 668 TCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCATCGACAG 727
Qy 728 AAGCACTGCTCTCTTGGTTTCAGACAAAGTCACGGAGAAAGAGCGTCTCTTGTTCCTCA 787
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Qy 788 TAAGAGCTCAAGAACAGCAATGTGATCGCTTCCAAAATGGGCTTCTCTCCCACTCAG 847
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Db 1088 AGCGCTTTCAAAAGGCTTCTTGAANAATATTTGTATATAAAAGCAACCTCTACCATCAC 1147
Qy 1148 ACACCG 1154
Db 1148 AACACAG 1154

RESULT 7

US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Query Match 57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACAAATCGCTTAAACATCAATTAATACTAAGCACTCGTTACTTTAGCATTTTATATGCTT 67
Db 11 CTAATAGCACAAATCAATTTATCTAAGCACTCGTTACTTTAGCATTTTATATGCTT 70

Qy 68 TACTAGCTATTGCTATTAATGTTAGGCATGCTGGTCAATTTAGCTTTTATATGTCGACA 127
Db 71 TAGTAGCTTTTGTCTATAAAGCTTAGGAAATCTTTGGTCAATTTTATGCTTTGTCGACA 130

Qy 128 GAAATCTTACACATCGAAGTAAATTTACTTTTCTTAATCTTGGCCATTCAGACATTTCTTTG 187
Db 131 AAAACCTTACACATCGAAGTAAATTTTCTTAATCTTGGCCATTCCTGACATTTCTTTG 190

Qy 188 TGGGTGCAATTTGCAATTCCTCTGTACATACCTTCCTCGCTGACTTACTGGAATTTCTGAA 247
Db 191 TGGGTGCAATTCCTCAATTCCTTTGTACATCCCTCACACGCTGTTTGGATGGGATTTTGGAA 250

Qy 248 AGCAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAGCATCTGTGTATA 307
Db 251 AGGAAATCTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAGCATCTGTGTATA 310

Qy 308 ATATTGCTCTCATCAGCTACGATCGCTACCAATCGAGTCTCAAAATGCCGTGTGGTATAGAG 367
Db 311 ACATTGCTCTCATCAGCTATGATCGATCTGCTGAGTCTCAATGCTGTGTCTTATAGAA 370

Qy 368 CTCAGCATCTGCGACCTGGAAATGCTACTCAGATGGTGGCTTTTGGATATTTCTCT 427
Db 368 CTCAGCATCTGCGACCTGGAAATGCTACTCAGATGGTGGCTTTTGGATATTTCTCT 427

Db 371 CTCACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGTTGGGTGCTGGCCT 430
Qy 428 TCATGACAAATGGGCGGATGATCTTGATTTTCAAGATCTTGGCAGAAATAGCACTACAGAAAT 487
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Qy 488 GTGACCTGGATTTTAAAGTGTGCTTCTCCCTACATCAATTTATTTGAATTC 547
Db 491 GTGAACCTGGATTTTTCGGATGGTATACCTCTTGGCATCATCTTCTGGATTCG 550
Qy 548 TGATCCCATCTTGTAGTGTCTTATTTTTCAGCGCCCATATTTTACTGAGCCTCTGGAGAC 607
Db 551 TGATCCCATCTTGTAGTGTCTTATTTTCAACATGAATTTATTTGGAGCCTGTGGAGC 610
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Db 668 TCTGTGGACACTCATTCAGAGTAGACTATCTTCAAGGAGATCTCTTCTGATCGACG 727
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Db 848 ATTCGTAGCTCTTCCACCAAGGAGCAATGTTGAATCTCTTAGAGCCAGGAGATTAGCCA 907
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Db 908 AGTCACTGGCATACTCTTAGGCTTTTGGCTTTGCTGGGCTTCCATATTCAGTACTA 967
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Db 1088 AGCGCTTCAAGAGCTTCTTGAATACTTCTGTAAGAGGCAATCCAGCCACCAC 1147
Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 8
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Re
; FILE REFERENCE: ARN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
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; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
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; PRIOR FILING DATE: 1999-05-28
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
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; PRIOR APPLICATION NUMBER: 60/156,634
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; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-13

Query Match 57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
Qy 8 CAATAACAGTACATCGCTTACATCAATAAAATTTCTTTCACATTTTATATGTCCT 67
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Db 11 CTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTATCTTTAGCAATTTTTATGTCCT 70
Qy 68 TACTAGCTATTGCTATTAATGTTAGGCAATGCGGTGTCATTTTAGCTTTTATTTGTGGACA 127
Db 71 TAGTAGCTTTTGCTATTAATGCTAGGAATGCTTTGGTCAATTTTAGCTTTTGTGGTGACA 130
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Db 191 TGGGTGTGATCTCCATCTTTGTACATCCCTCACAGCTGTTTGGAAATTTTGGAA 250
Qy 248 AGCAAGCTTTGTAATTTTGGCTCAATTAAGTCAATCTTTTATGTAAGCACTGCTGTATATA 307
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Db 611 GTGATCATCTCAGTAGGTGCCAAAGCCATCTGAGACTGACTGCTCTCTTCCAAACA --- 667
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Qy 848 ATTCCCTGGCTCTTCAAGAAAGGAAACATATCGAACTTTTCAAGCCAGGAAATAGCCA 907
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Db 1028 CATTTTGGCTTCAGTGGTTCAATTTCTTGTGCAATCTCTTGTGATCCATTTGTTGTCACA 1087
Qy 1088 AACGTTTTCAAGAGGCTTTCTGAAATATCTTCTGTGAGAGGCAATTCACGCCACAC 1147
Db 1088 AGCGTTTTCAAGAGGCTTTCTTGAATATATTTTGTATAAAAAAGCAACCTCTACCATCAC 1147
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Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154
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RESULT 9
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1
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Query Match 57.7%; Score 675; DB 5; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
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Qy 8 CAAATACAGTACAAATCGCCTTAACATCAATTAATAATTTCTTTGACATTTTAAATGTCCT 67
Db 11 CTAAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCAATTTTATGTCCT 70
Qy 68 TACTAGCTATTGCTATTAATGTTAGGCAATGCTCGTGTGCTATTTAGCTTTTATTTGTGGACA 127
Db 71 TAGTAGCTTTTGCTATTAATGCTAGGAATGCTTTTGGTCAATTTTAGCTTTTGTGGTGACA 130
Qy 128 GAAATCTTAGACATCGAAGTAATTTACTTTTTCTTAACCTTGGCCATTTGCAAGCTTCTTTG 187
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Qy 248 AGCAAGCTTTGTAATTTTGGCTCAATTAAGTCAATCTTTTATGTAAGCACTCTGTGTATA 307
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Qy 368 CTCAGCACTCTGGCACTGGAAATTTGCTACTCAGATGGTGGCTGTTTGGATATTTCTCT 427
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Db 491 GTGAACCTCGAATTTTTCGGAATGGTACATCTCTTGGCCATCAATCTTGGAAATCG 550
Qy 548 TGATCCCACTCTGTTAGTGTCTTATTTCAAGCCCCATATTTACTGAGGCTGTGGAGC 607
Db 551 TGATCCCACTCTGTTAGTGTCTTATTTCAACATGAATATTTTATTTGGAGCTGTGGAGC 610
Qy 608 GAGGAAATCTGAGCAGGCTGCTGAGCCAGCTGCTGCTCCCTGCTGACTCTTCCAGCAGTG 667
Db 611 GTGATCATCTCAGTAGGTGCCAAAGCCATCTGAGACTGACTGCTCTCTTCCAAACA --- 667
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Db 908 AGTCACCTGGCCATCTCTCTAGGGGTTTTGCTGTTTGTCTGGGCTCCATATCTCTCTGTCA 967
Qy 968 CAGTTATCTACTCATTTTTTCTGAAAGAACTTGACATAAATCAACCTGGTACCATACTG 1027
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Qy 1028 CTTTGTGGCTCCAGTGGTTCAATTTCTTTGTTAAATCCCTTTTTTGTATCCATTTGTGTGACCA 1087
Db 1028 CATTTGGCTTCAGTGGTTCAATTTCTTTGTCAATCCCTCTTTTGTATCCATTTGTGTGACCA 1087
Qy 1088 AACGTTTTCAGAGGCTTTCTGAAAAATATCTCTGTGAGAGGAATCCACGCCACAC 1147
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Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 11
US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PCL0373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Query Match 57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAATTAACAGTACAAATCGCCCTTAACATCAATTAATAATTTCTTTGACATTTTAAATGCTT 67
Db 11 CTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTTTATGTCCT 70
Qy 68 TACTAGCTATTGCTATATATGTTAGCAATGCTGCTCATTTAGCTTTTATTTAGTGACCA 127
Db 71 TAGTAGCTTTTGTATATATGCTAGGAATGCTTTGGTCATTTTATGCTTTTGTGTGACCA 130
Qy 128 GAAATCTTTAGACATCGAAGTAAATTAATTTTCTTAACCTTGGCCATTTGACACTCTTTG 187
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Qy 428 TCATGACAAATGGGCCGAGATTTCTGATTTTCAAGCTCTTGGCAGAAATPAGCACTACAGAA 487
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Db 611 GTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGTCTCTCTTCCAACA- 667
Qy 668 ACCAGGACACTCTCTGAGACAGACCCCGATTTCAAGGGCGACTCTGCCAGCAGCGGAAG 727
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Db 1088 AGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATAAAAAAGCAACCTCTACCATCAC 1147
Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 12
US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044

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; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-393-807-13

Query Match      57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7,5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATAACAGTACCAATCGCCCTTAACATCAATATAAAATTTCTTTGACATTTTAAATGCTT 67
Db 11 CTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTTTATGCTCT 70

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Qy 608 GAGAAACCTGAGCAGGTGGCTTCAGCCACCTCTGACTCTCCCTCTGACTCTTCCAGCAGTG 667
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; Sequence 13: Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7 US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match      57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACGATCGCCTTAACATCAATTAATAATTTCTTGCACATTTTAAATGCTT 67
Db 11 CTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTTTATGTCCT 70

Qy 68 TACTAGCTATTGCTATATAGTATAGCAATGTCGGTCAATTTTAGCTTTTATTGTGGACA 127
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; PRIOR APPLICATION NUMBER: 10349253A-1
; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergema, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-349-253A-1

Query Match      57.7%; Score 675; DB 7; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACGATCGCCTTAACATCAATTAATAATTTCTTGCACATTTTAAATGCTT 67
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US-10-723-955-13

; Sequence 13, Application US/10723955

; Publication No. US20040110238A1

; GENERAL INFORMATION:

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; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liao, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
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; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

; FILE REFERENCE: 7 US29 CON

; CURRENT APPLICATION NUMBER: US/10/723,955

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 10/417,820

; PRIOR FILING DATE: 2003-4-16

; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: 60/110,060

; PRIOR FILING DATE: 1998-11-27

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,852

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/123,944

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,945

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,948

; PRIOR FILING DATE: 1999-03-12

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-955-13

Query Match 57.7%; Score 675; DB 7; Length 1173;

Best Local Similarity 74.9%; Pred. No. 7.5e-185;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACAAATCGGCTTAAATCAATTAATTTCTTTGACATTTTAAATGCTT 67

Db 11 CTAATAGCAATCAATTTATCTAAGCACTGCTGTTACTTTTAGCATTTTATGTCCT 70

Qy 68 TACTAGCTATGCTATAATAGTTAGGCAATGCTGCTGTCATTTTATGTCGACA 127

Db 71 TAGTACTTTTGTCTATAATGCTAGGAAATGCTTTGTCATTTTAGCTTTTGTGTCGACA 130

Qy 128 GAAATCTTAGACATCGAAGTAATTTACTTTTCTTAACCTTGGCCATTTGACACTTCTTTG 187

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OM nucleic - nucleic search, using sw model

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Title: US-10-626-398-7

Perfect score: 1170

Sequence: 1 atgttgcaataacagctac.....acgctcaatccacttga 1170

Scoring table: IDENTITY NUC

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	675	57.7	1173	3	US-09-812-216-1
3	675	57.7	1173	3	US-09-875-076-13
4	132.2	11.3	1239	3	US-09-891-053-2
5	132.2	11.3	2700	3	US-09-891-053-5
6	123	10.5	1338	3	US-09-165-543-6
7	123	10.5	1953	3	US-09-891-053-26
8	123	10.5	3244	3	US-09-165-543-4
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13	110.2	9.4	1335	3	US-09-642-514-6
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32	73	6.2	1956	3	US-08-767-993-6	Sequence 6, Appli
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42	63.2	5.4	1893	3	US-09-891-053-13	Sequence 13, Appli
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45	55.4	4.7	1554	2	US-08-031-538-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monama, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Query Match	57.7%	Score 675;	DB 3;	Length 1173;
Best Local Similarity	74.9%	Pred. No. 4.4e-203;		
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Db 1088 AGCGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAAGCACTCTACCATCAC 1147
Qy 1148 AACACCG 1154
Db 1148 AACACAG 1154

RESULT 3

US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, i-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280

; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Query Match 57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 4.4e-203;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATAACAGTACCAATCGCCTTAAATCAATCAATTTTCTTAACTTGGCCATTTTGAATTTTAAATGCTT 67
Db 11 CTAATAGCACAAATCAATTTTATCATAAGCACTCGTGTACTTTAGCAATTTTATGCTCT 70

Qy 68 TACTAGCTATGCTATTAATGTTAGGCAATGCTGGTCAATTTTACCTTTTATTTAGCTTTTATTTGGACA 127
Db 71 TAGTAGCTTTTGTCTAATGCTAGGAAATGCTTTGGTCAATTTTATTTAGCTTTTGTGGTGGACA 130

Qy 128 GAAATCTTAGACATCGAAGTAATTTACTTTTCTTAACTTGGCCATTTGACACTTCTTTG 187
Db 131 AAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCTGACTTCTTTG 190

Qy 188 TGGGTGCAATTTGCAATTTCTCTGTATACATACCTCTCTCGTGAATTTTACCTTTCTTGGAA 247
Db 191 TGGGTGTGATCTCCATTTCTTTGTATACATCCCTCACACGCTGTTCCGAATGGGATTTTGGAA 250

Qy 248 AGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATTTATGTACAGCATCTGTGTATA 307
Db 251 AGGAAATCTGTGTATTTTGGCTCATCTACTGACTATCTGTTATGTATACAGCATCTGTATATA 310

Qy 308 ATATTGTCTCATCAGCTACGATCGTACCAGTACAGTCTCAATGCGGTGGTGTATAGAG 367
Db 311 ACATTGTCTCATCAGCTATGATCGATACCTGTGAGTCTCAATGCTGTGTATAGAA 370

Qy 368 CTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTTGGATATTTCTCT 427
Db 371 CTCACATACCTGGGGTCTTGAAGATTTTACTCTGTATGGTGGCGCTTTGGGTGCTGGCT 430

Qy 428 TCATGACAAATGGGCGCATGATTTCTGATTTTCAAGTCTTGGCAGATAGCACTACAGAT 487
Db 431 TCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAGGATGAAGTGTAGTGAAT 490

Qy 488 GTGAACCTGGATTTTAAAGGTTGTTGCTCTCCCTACATCATATTTTGAATTTCC 547
Db 491 GTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCATCATCTCTTGGATTCG 550

Qy 548 TGATCCCCATCTTGTAGTTGCTTTATTTTCAGCGCCCATATTTTACTTGGAGCTGTGGAGC 607
Db 551 TGATCCCCAGTCACTTAGTCGCTTATTTTCAACATGAATATTTTATTTGGAGCTGTGGAGC 610

Qy 608 GAGAGAACTGAGCAGGTGCTCTAGCCACCTGTACTCCCTCTGACTCTTCTCCAGCAGTG 667
Db 611 GTGATCATCTCAGTAGGTGCCAAAGCCATCTGAGCTGACTGTCTCTCTTCCAAACA --- 667

Qy 668 ACCACGACACTCTCTGAGCAGGAGCCCGGATTTCAAGGCGGACTCTGCGCAGCAGGAAG 727
Db 668 TCTGTGACACTCTCAATCAGAGGTAGATATCTTCAAGGAGATCTCTTTCTGCATCGACAG 727

Qy 728 AACCAACTGCTCTCTTGGTTTCAGACCAAGTCAACGAGAGAAAGAGCAGTCTCTTTGTTTCCA 787
Db 728 AAGTTCTGTGATCTTTTCAATTCAGAGAGACAGAGAGAAAGAGTAGTCTCATGTTTCTCT 787

APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2700
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (351)...(1589)
NAME/KEY: misc feature
LOCATION: (1)...(2700)
OTHER INFORMATION: n = A,T,C or G

US-09-891-053-5

Query Match 11.3%; Score 132.2; DB 3; Length 2700;
Best Local Similarity 48.7%; Pred. No. 7.3e-31;
Matches 523; Conservative 0; Mismatches 528; Indels 24; Gaps 5;

Qy 59 TAAATGCTTTACTAGTATGCTATAATGTTAGGCAATGTCGTCTATTTCAGCTTTTA 118
Db |||||
Qy 469 TCATGGCGCTGCTCATGTGGCCACAGTACTGGGCAACGCGCTGTCATGTCGCCCTCG 528
Db |||||
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACTTGGCCATTGCAG 178
Db |||||
Qy 529 TGGCGGATTCAGAGCTCCGCCACAGAACAACTTCTTCTGCTCAACTCGCCATCTCG 588
Db |||||
Qy 179 ACTTCTTTGGGGTGCAATTCCTCTGTATACATCTTCTGTCAGTCTTCTGTCAGTCTAC 235
Db |||||
Qy 589 ACTTCTCTGGTGGCTCTCTGCACTCCCAATGTACGTACCTATGTGTGACCGCGCTT 648
Db |||||
Qy 236 GGACTTCTGNAACAGCTGTGTATTTGGCTCATTAAGTACTGATCTTTTATGTACAG 295
Db |||||
Qy 649 GGACCTTTCGGCGGGGCTCTGCAAGCTGTGGCTGGGTAGACTACTTACTGTGTGCT 708
Db |||||
Qy 296 CATCTGTATAATATTTCTCTCATCAGCTACGATCGTACAGTCTGCTCAAAATGCG 355
Db |||||
Qy 709 CTTGGTCTTCAACATGTACTCATCAGTATGACCGATTCCTGTAGTCTACTGAGCTG 768
Db |||||
Qy 356 TGTGGTATAGAGCTCAGACCTCTGGCACCTGGCAAAATGCTACTCAGATGGTGGCTTT 415
Db |||||
Qy 769 TCTCTCAGGGCCAGCAGGGGGACACGAGCGGGCGCTTCGGAAGATGGCACTGGTGT 828
Db |||||
Qy 416 GGATATTTCTCTTATGACAAATGGCGGATGATTTCTGATTTTCAGACTCTTGGCAGATA 475
Db |||||
Qy 829 GGGTGTGGGCTTCTCTGTATGGGCTGTCGATCTTCTGAGTGGAGTACTGCTGTGGTG 888
Db |||||
Qy 476 GCATACAG-----AATGTGAACCTGGAATTTTAAAAAGTGGTACTTTTGTCTC 523
Db |||||
Qy 889 GCAGTTCAATCCCGAGGGCCACTGTATGCTGAGTCTTCTACACTGGTACTTTCTCA 948
Db |||||
Qy 524 TCCCTACATCATTTATGGAATTCCTGATCCCAATCTTTTGTAGTTGCTTTATTCAGCGCCC 583
Db |||||
Qy 949 TCAGGGCTCCACCTCGAGTTCTTCAGCGCTTCTCAGCGTTTACCTTCTTCAACTCA 1008
Db |||||
Qy 584 ATATTTACTGAGCTGTGGAGCGAGAGAACTGAGAGGTGCTCAGCCACCTGTAC 643
Db |||||

Db 1009 GCATCTACTGAACATCCAGAGGGCCACCCGCTTTCGGCTTGTATGGGGCGGTGAGGCTG 1068
Qy 644 TCCCTCTGACTCTTTCAGAGAGTGAACACAGGACACTCTCTGAGAGAGAGAGAGAGAGAG 703
Db |||||
Qy 1069 GCCAGGAACCC-----CCACAGAGATGCCAGCCCTCGCCACCTCCAGAGCTCCCGCCAGCTGC 1124
Db |||||
Qy 704 GGGGACTCTGCGCAGCAGGGAAGAAACAACTGCTCTCTTGGTTTCAGACAAGTCAACGGA 763
Db |||||
Qy 1125 TGGGGCTGTGGCCAAAGGGCATGGGAGGCGCATGGCTTTCAGAGCTCTGGGAGCTCC 1184
Db |||||
Qy 764 GAAAGAGCAGTCTCTTCTTTTTCATAAGAGGCTTCAAGAAACAGCAATGTGTATCGCTTCCA 823
Db |||||
Qy 1185 TCAAGGGGCACTGAGAGGCCACGCTCACTCAAAAGGGGCTCCAAAGCCATCAGCATCTTCA 1244
Db |||||
Qy 824 AATGGGCTTCTCTCTCCACTCAGATTCCTTGGCTCTTTCAGCAAGAGGAAATATTCGAAC 883
Db |||||
Qy 1245 GCATCCCTGGAGAGCGCATGAAGATGTGTCTCCAGAGCATC--ACCAGGCTTTCGGC 1302
Db |||||
Qy 884 TTTTCAGAGCCAGGAATTAGCCAAGTCACTGGGCCATCTTTCAGAGCTTTTTCGCAATTT 943
Db |||||
Qy 1303 TGTGGGGCAAGAGAGGTGGCCAAAGTGGCTGCGCATCATCGTAGCATCTTTTGGGCTCT 1362
Db |||||
Qy 944 GCTGGGCTCCATATTCATGACTACAGTATCTACTCATTTTCTTCTGAAAGGAATTTGA 1003
Db |||||
Qy 1363 GCTGGGGCGGTACACGCTCTCTAATGATCATCCGAGCTGTGTCATGGCCGCTGCATCC 1422
Db |||||
Qy 1004 CTAATCAACCTGGTACCATCTGCTTTGGCTTCCAGTGGTTCATTTCTTTTGTAAATC 1063
Db |||||
Qy 1423 CCGATT---ACTGGTACGAGAGCTCTTCTGGCTTCTGTGGGCCAACTCGGCCGCTCAACC 1479
Db |||||
Qy 1064 CTTTGTATCCATTTGTGTCAAAAGCTTTTTCAGAGGCTTTTCTGAAATACT 1118
Db |||||
Qy 1480 CCGTCTCTACCCACTGTGCCACTACAGCTTCGCGAGAGGCTTCCACCAAGCTCT 1534
Db |||||

RESULT 6

US-09-165-543-6
Sequence 6, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-09-165-543-6

Query Match 10.5%; Score 123; DB 3; Length 1338;
Best Local Similarity 54.0%; Pred. No. 3.9e-28;
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;
QY 59 TAATGCTCTTACTAGCTATTGCTATAATGTTAGGCAATGCTGGTCAATTTTACGCTTTTA 118
Db 119 TCATGGCGCTGCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTCACTGCTGCCTTCG 178
QY 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTGGCCATTCGAG 178
Db 179 TGGCGGATTGCGAGCTCCGACACCAGAACTTCTTTCTGCTCAACCTGCCATCTCG 238
QY 179 ACTTCTTTGGGTGGCAATTCCTCTGTACATACCTTCTCGCTGACTTAC---T 235
Db 239 ACTTCTCTGGGTGGCTTCTGCAATCCATTTGACGTACCTATGCTGACCGGCCGTT 298
QY 236 GGACTTCTGAAAGCAAGCTTGTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAG 295
Db 299 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGTGGTAGACTACTTACTGTGCTT 358
QY 296 CATCTGTGTATAATTTGCTCTCATCAGCTACGATCGCTACCAAGTCACTTCAAATGCCG 355
Db 359 CCTCGGCTTCAACATCGTACTCATCAGTATGACCGATTCTCTGCTCACTCGAGCTG 418
QY 356 TGTGGTATAGAGCTCAGCACTCTGGACCTGGCACTGGAATTTGCTATCAGATGGTGGCTGTT 415
Db 419 TCTCTCAGGGGCCAGCAGGGGGACACGAGCGGGCGCTTCGGAAGATGGCACTGGTGT 478
QY 416 GGAATTTCTCTTCATCAGAAATGGGCGCATGATTCGATTTCAGACTCTTTGGCAGAATA 475
Db 479 GGGTGTGGCTTCTCTGCTGTATGGGCTGCGCATCTCTGAGTTGGAGTACTGTCTGGTG 538
QY 476 GCACTACAG-----AATGTGAACCTGGAATTTTAAAGTGGTACTTTGCTC 523
Db 539 GCACTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGTTCTTCTCA 598
QY 524 TCCCTACATCAATTTGGAATTCCTGATCCCATCTTTGTTAGTGTCTATTTCAGGCC 593
Db 599 TCAGGGCTCCACCTCGAGTTCTTTCAGGCCCTTCTCAGCGCTTACCTTCTCAACCTCA 658
QY 584 ATATTACTGGAGCTGTGGAAGCG 608
Db 659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 7

US-09-891-053-26

; Sequence 26, Application US/09891053

; Patent No. 6750322

; GENERAL INFORMATION:

; APPLICANT: Itadani, Hiraku

; APPLICANT: Takimura, Tetsuo

; APPLICANT: Nakamura, Takao

; APPLICANT: Kobayashi, Masahiko

; APPLICANT: Tanaka, Ken-ichi

; APPLICANT: Hidaka, Yusuke

; APPLICANT: Ohta, Masataka

; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

; FILE REFERENCE: 06501-083001

; CURRENT APPLICATION NUMBER: US/09/891,053

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: PCT/JP99/07280

; PRIOR FILING DATE: 1999-12-24

; PRIOR APPLICATION NUMBER: PCT/JP98/05967

; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1953
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (302)...(1636)
US-09-891-053-26

Query Match 10.5%; Score 123; DB 3; Length 1953;
Best Local Similarity 54.0%; Pred. No. 4.9e-48;
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;
QY 59 TAATGCTCTTACTAGCTATTGCTATAATGTTAGGCAATGCTGGTCAATTTTACGCTTTTA 118
Db 420 TCATGGCGCTGCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTCACTGCTGCCTTCG 479
QY 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTGGCCATTCGAG 178
Db 480 TGGCGGATTGCGAGCTCCGACACCAGAACTTCTTTCTGCTCAACCTGCCATCTCG 539
QY 179 ACTTCTTTGGGTGGCAATTCCTCTGTACATACCTTCTCGCTGACTTAC---T 235
Db 540 ACTTCTCTGGGTGGCTTCTGCAATCCATTTGACGTACCTATGCTGACCGGCCGTT 599
QY 236 GGACTTCTGAAAGCAAGCTTGTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAG 295
Db 600 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGTGGTAGACTACTTACTGTGCTT 659
QY 296 CATCTGTGTATAATTTGCTCTCATCAGCTACGATCGCTACCAAGTCACTCAAATGCCG 355
Db 660 CCTCGGCTTCAACATCGTACTCATCAGCTATGACCGATTCTCTGCTCAGTCACTCGAGCTG 719
QY 356 TGTGGTATAGAGCTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTT 415
Db 720 TCTCTACAGGGGCCAGCAGGGGACACGAGACGGCGCTTCGGAAGATGGCACTGGTGT 779
QY 416 GGAATTTCTCTTCATGACAAATGGGCGCATGATTTCTGATTTTCAGACTCTTTGGCAGAATA 475
Db 780 GGGTGTGGCTTCTCTGCTGTATGGGCTGCCATCTCTGAGTTGGAGTACTCTGTCTGGTG 839
QY 476 GCACTACAG-----AATGTGAACCTGGAATTTTAAAGTGGTACTTTGCTC 523
Db 840 GCACTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTCTCA 899
QY 524 TCCCTACATCAATTTGGAATTCCTGATCCCATCTTTGTTAGTGTCTATTTCAGGCC 583
Db 900 TCAGGGCTCCACCTCGAGTTCTTTCAGGCCCTTCTCAGCGCTTACCTTCTCAACCTCA 959
QY 584 ATATTACTGGAGCTGTGGAAGCG 608
Db 960 GCATCTACCTGAACATCCAGAGCG 984

RESULT 8

US-09-165-543-4

; Sequence 4, Application US/09165543

; Patent No. 6093545

; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann

; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 778..2112
US-09-165-543-4

Query Match 10.5%; Score 123; DB 3; Length 3244;
Best Local Similarity 54.0%; Pred. No. 6.7e-28;
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;
Qy 59 TAATGCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTCATTTTACCTTTTA 118
Db 896 TCATGGGCGTCTCATCGTGGCCACGACTGAGTGGGCAACGGCTGCTATGCTGCGCTCG 955
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAACTTTTCTTAACTTGGCCATTGCG 178
Db 956 TGGCGGATTGAGGCTCGGACCCAGAACAACTTTCTGCTCAACTGCGCATCTCG 1015
Qy 179 ACTTCTTTTGGGGTGCATTTGCAATTCCTCTGTATACATCTTCTGCTGACTTAC---T 235
Db 1016 ACTTCTCTGTTGGTGGCTTCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Qy 236 GGACTTCTGGAAGCAAGCTTGTGTATTTTGGCTCATCTAGCTATCTTTTATGTACAG 295
Db 1076 GGACTTCTGCGCGGGGCGCTCTGCAAGCTGTGGCTGTGGTGTAGACTACTACTGTG 1135
Qy 296 CATCTGTATTAATTTGCTCTCATCAGCTACGATCGTACCGTACGCTGCTCAAAATCGG 355
Db 1136 CCTCGGCTTCAACATGCTACTCATCAGCTATGACCGATTCCTGCTGCTGCTGCTGCTG 1195
Qy 356 TGTGCTATAGAGCTCAGCACTCTGGCACCTGGAATAATGCTACTCAGATGCTGCTGTT 415
Db 1196 TCTCTACAGGCGCCAGCAGGGGACACGAGCGGCGCTTGGGAAGATGCGACTGCTGT 1255
Qy 416 GGATATTTCTCTCATGACAAATGGGCGGATGATTTGATTTTCAAGCTCTTTGGCAGATA 475
Db 1256 GGGTGTGGGCTTCTGCTGTATGGGCTGCGCATCTGAGTTGGGAGTACCTGCTGCTGTG 1315
Qy 476 GCATACAG-----AATGTGAACCTGGATTTTAAAGAGTGGTACTTTGCTC 523
Db 1316 GCAGTTCCATCCCGAGGCGCACCTGCTATGCTGAGTTCTTCAACTGGTACTTTCTCA 1375
Qy 524 TCCCTACATCATTTATGGAATTTCTGATCCCGCATCTGTTAGTTGCTTTATTTAGCGGCC 583
Db 1376 TCAGGGCTCACCTCGAGTTCTTCAAGCGCTTCTCAGCGCTTCTCAGCGTTACCTTCTT 1435
Qy 584 ATATTTACTGGAGCCTGTGGAAGCG 608

Db 1436 GCATCTACCTGAACATCCAGAGCG 1460
RESULT 9
US-08-985-090-3
Sequence 3, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-08-985-090-3

Query Match 9.4%; Score 110.2; DB 2; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.5e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
Qy 59 TAATGCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTCATTTTACCTTTTA 118
Db 119 TCATGGGCGTCTCATCGTGGCCACGGCTGCTGGGCAACGGCTGCTATGCTGCGCTCG 178
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAACTTTTCTTAACTTGGCCATTGCG 178
Db 179 TGGCGGACTCGAGCTCGGACCCAGAACAACTTTCTGCTCAACTGCGCATCTCG 238
Qy 179 ACTTCTTTTGGGGTGCATTTGCAATTCCTCTGTATACATCTTCTGCTGCTGCTGCT 235
Db 239 ACTTCTCTGCTGGGCGCTTCTGCAATTCCTGCTATGCTGCTGCTGCTGCTGCTGCTG 298
Qy 236 GGACTTCTGGAAGCAAGCTTGTGTATTTTGGCTCATCTAGCTATCTTTTATGTACAG 295
Db 299 GGACTTCTGGCGGGGCGCTCTGCAAGCTGTGGTGGTAGTGACTACTCTGCTGCGACCT 358
Qy 296 CATCTGTATTAATTTGCTCTCATCAGCTACGATCGTACCGTACGCTGCTCAAAATCGG 355
Db 359 CCTCTGCTTCAACATGCTGCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCT 418

356 TGTGTATAGAGCTCAGCACTCTGGCACTCGGCAAAATTTGCTACTCAGATGGTGGCTGTTT 415
119 TCATGGCGTCTCTCATCTGGCCACGGTGTCTGGGCAACGGCTGGTCTATGCTCGCCTTCG 178
119 TTCTGGACAGAAATCTTAGACATCGAAGTAATTTACTTTTTTCTTAAGTGGCCATTGCGAG 178
179 TGCCGACATCGAGCCCTCGGCACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCG 238
179 ACTTCTTTTGTGGTGCAATTTGCAATTTCTCTGTATACATACCTTCTCTCGCTGAC---TTACT 235
239 ACTTCTCTGTCTGGCGCTTCTGATCCCACTGTATGTACCTACGTGTGACAGCGCGCT 298
236 GGAATTTCTGGAAGAGAGCTTTGATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295
299 GGAATTTCTGGAAGAGAGCTTTGATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 358
296 CATCTGTGTATATATTTGCTCTCATCAGCTACCATCGCTACAGTCTCAGTCTCAAAATGCGG 355
359 CCTCTGCTTCAACATCGTGTCTCATCAGCTACCATCGCTTCTCTGCTGCTCAGCGAGCGG 418
356 TGTGTATAGAGCTCAGCACTCTGGCACCTCTGGCACTTGGTGTGCTACTCAGATGGTGGCTGTTT 415
419 TCTCATACCGGCGCCAGAGGCTGACACGGCGGGCAGTGGCGAAGATGCTGTGTGT 478
416 GGAATTTCTTCTTATGACAAATGAGGCGGAGATTTCTGATTTTCAAGTCTTTGGGAGATA 475
479 GGGTGTCTGGCTTCTCTGTATACGACCACTCTGAGCTGGGAGTACCTGTCCCGGG 538
476 GCACTAC-----AGAAATGCAACTGGATTTTAAAGTGGTGTACTTTGCTC 523
539 GCAGCTCAATCCCGAGGCGCACTGTCGCGAGTCTTCTTCAACCTGGTACTTCTCA 598
524 TCCCTACATCATTTATTTGGAATTTCTGATCCCGCACTTTGTTAGTGTCTTATTTAGCGGCC 583
599 TCAAGGCTTCCACCTTGGAGTCTTTTACGCGCTTCTCAGCGTCACTCTTTTAACTCA 658
584 ATATTACTGGAGCTGTGGAAGCG 608
659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 10

US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-3

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.5e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
59 TAATGCTTTTACTAGCTATTGCTATATGTTAGGCAATGTCGTGGTCAATTTTACTGCTTTTA 118

119 TCATGGCGTCTCTCATCTGGCCACGGTGTCTGGGCAACGGCTGGTCTATGCTCGCCTTCG 178
119 TTCTGGACAGAAATCTTAGACATCGAAGTAATTTACTTTTTTCTTAAGTGGCCATTGCGAG 178
179 TGCCGACATCGAGCCCTCGGCACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCG 238
179 ACTTCTTTTGTGGTGCAATTTGCAATTTCTCTGTATACATACCTTCTCTCGCTGAC---TTACT 235
239 ACTTCTCTGTCTGGCGCTTCTGATCCCACTGTATGTACCTACGTGTGACAGCGCGCT 298
236 GGAATTTCTGGAAGAGAGCTTTGATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295
299 GGAATTTCTGGAAGAGAGCTTTGATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 358
296 CATCTGTGTATATATTTGCTCTCATCAGCTACCATCGCTACAGTCTCAGTCTCAAAATGCGG 355
359 CCTCTGCTTCAACATCGTGTCTCATCAGCTACCATCGCTTCTCTGCTGCTCAGCGAGCGG 418
356 TGTGTATAGAGCTCAGCACTCTGGCACCTCTGGCACTTGGTGTGCTACTCAGATGGTGGCTGTTT 415
419 TCTCATACCGGCGCCAGAGGCTGACACGGCGGGCAGTGGCGAAGATGCTGTGTGT 478
416 GGAATTTCTTCTTATGACAAATGAGGCGGAGATTTCTGATTTTCAAGTCTTTGGGAGATA 475
479 GGGTGTCTGGCTTCTCTGTATACGACCACTCTGAGCTGGGAGTACCTGTCCCGGG 538
476 GCACTAC-----AGAAATGCAACTGGATTTTAAAGTGGTGTACTTTGCTC 523
539 GCAGCTCAATCCCGAGGCGCACTGCTATGCGCGAGTCTTCTTCAACCTGGTACTTCTCA 598
524 TCCCTACATCATTTATTTGGAATTTCTGATCCCGCACTTTGTTAGTGTCTTATTTAGCGGCC 583
599 TCAAGGCTTCCACCTTGGAGTCTTTTACGCGCTTCTCAGCGTCACTCTTTTAACTCA 658
584 ATATTACTGGAGCTGTGGAAGCG 608
659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 11

US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-167-354-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.5e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
59 TAATGCTTTTACTAGCTATTGCTATATGTTAGGCAATGTCGTGGTCAATTTTACTGCTTTTA 118
119 TCATGGCGTCTCTCATCTGGCCACGGTGTCTGGGCAACGGCTGGTGTGCTGCTCGCTTCG 178
119 TTCTGGACAGAAATCTTAGACATCGAAGTAATTTACTTTTTTCTTAAGTGGCCATTGCGAG 178

Db 179 TGGCGACTCGAGCTCCGACCCAGACAACTTCTTCTGCTCAACCTCGCCATCTCCG 238
Qy 179 ACTTCTTTGGGTGGAATTCGAATTCCTCTGTATACATACCTTCTCGGTGAC---TTACT 235
Db 239 ACTTCTCGTGGGGCCCTTCTGCAATCCACATGATGATACCTTGTGACAGGCCGCT 298
Qy 236 GGACTTCTGGAAAGCAAGCTTGTGATATTTTGGCTCATCTACTGACTATCTTTATGTACAG 295
Db 299 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTGCTGTGCACCT 358
Qy 296 CATCTGTGTATAATATTTCTCATCTAGCTACGATCGCTACAGTCACTCTCAAAATGCG 355
Db 359 CCTCTGCTTCAACATCTGTCTCATCTAGCTACGACCGCTTCTGTGTGACCGAGGG 418
Qy 356 TGTGGTATAGAGCTCAGACACTCTGGCACCTGGAAAATTTGCTACTCAGATGGTGTCTTT 415
Db 419 TCTCATACCGGGCCAGCGGGTGACACGGCGGCGAGTGCAGAAAGATGCTGTGTGT 478
Qy 416 GGATATTTCTCTTCATGACAAATGGCGGATGATTTCTGATTTTCAGACTCTTTGGCAGAATA 475
Db 479 GGGTGTGGCTTCTCTGTCTGTACGGACCGACCATCTCTGAGCTGGAGTACCTGTCCGGGG 538
Qy 476 GCACTAC-----AGAAATGTGAACCTGGATTTTAAAAAGTGTACTTTTGCTC 523
Db 539 GCAGCTCCATCCCGAGGGCCACTGTATGCGAGTCTTCTCAACACTGGTACTTCTCA 598
Qy 524 TCCCTACATCATTAATGGAATTCCTGATPCCCATCTTGTGTAGTGTCTTATTTACGCGCC 583
Db 599 TCAGGGCTTCACCTGGAGTCTTTAGCGCTTCTCTCAGCGTCACTCTTTTAACTCA 658
Qy 584 ATATTTACTGGAGCTGTGGAAGCG 608
Db 659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 12

US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.5e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
Qy 59 TAATGCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGGTCAATTTAGCTTTTA 118
Db 119 TCATGGCGCTCTCATCTGGCCACGGTGTGGGCAAGCGCTGTATGCTCGCCTTCG 178
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACTGGCCATTGCG 178
Db 179 TGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCG 238

Qy 179 ACTTCTTTGGGTGGAATTCGAATTCCTCTGTATACATACCTTCTCGGTGAC---TTACT 235
Db 239 ACTTCTCGTGGGGCCCTTCTGCAATCCACATGATGATACCTTGTGACAGGCCGCT 298
Qy 236 GGACTTCTGGAAAGCAAGCTTGTGATATTTTGGCTCATTTACTGACTATCTTTATGTACAG 295
Db 299 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTGCTGTGCACCT 358
Qy 296 CATCTGTGTATAATATTTCTCATCTAGCTACGATCGCTACAGTCTCAAAATGCGG 355
Db 359 CCTCTGCTTCAACATCTGTCTCATCTAGCTACGACCGCTTCTGTGTGACCGAGGG 418
Qy 356 TGTGGTATAGAGCTCAGACACTCTGGCACCTGGAAAATTTGCTACTCAGATGGTGTCTTT 415
Db 419 TCTCATACCGGGCCAGCGGGTGACACGGCGGCGAGTGCAGAAAGATGCTGTGTGT 478
Qy 416 GGATATTTCTCTTCATGACAAATGGCGGATGATTTCTGATTTTCAGACTCTTTGGCAGAATA 475
Db 479 GGGTGTGGCTTCTCTGTCTGTACGGACCGACCATCTCTGAGCTGGAGTACCTGTCCGGGG 538
Qy 476 GCACTAC-----AGAAATGTGAACCTGGATTTTAAAAAGTGTACTTTTGCTC 523
Db 539 GCAGCTCCATCCCGAGGGCCACTGTATGCGAGTCTTCTCAACACTGGTACTTCTCA 598
Qy 524 TCCCTACATCATTAATGGAATTCCTGATPCCCATCTTGTGTAGTGTCTTATTTACGCGCC 583
Db 599 TCAGGGCTTCACCTGGAGTCTTTAGCGCTTCTCTCAGCGTCACTCTTTTAACTCA 658
Qy 584 ATATTTACTGGAGCTGTGGAAGCG 608
Db 659 GCATCTACCTGAACATCCAGAGCG 683

RESULT 13

US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.5e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
Qy 59 TAATGCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGGTCAATTTAGCTTTTA 118
Db 119 TCATGGCGCTCTCATCTGGCCACGGTGTGGGCAAGCGCTGTATGCTCGCCTTCG 178
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACTGGCCATTGCG 178
Db 179 TGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCG 238
Qy 179 ACTTCTTTGGGTGGAATTCGAATTCCTCTGTATACATACCTTCTCGGTGAC---TTACT 235

Db 239 ACTTCTCGTGGCGCCTTCTGCATCCCACTGATGTACCTACGTCGACAGGCGCT 298
Qy 236 GGACTTCTGGAAGCAAGCTTGTGTAATTTGGCTCAATTAAGTATCTTTTATGTACAG 295
Db 299 GGACTTCTGGCGCGGGGCTCTGACAGCTGTGGCTGGTAGTGGAAGTACCTGCTGTGACCT 358
Qy 296 CATCTGTGTATATAATTTGCTCTCATCAGCTACGATCGCTACCAAGTCAAGTCTCAAAATGCGG 355
Db 359 CCTCTGCTTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCGTCAACCGAGCGG 418
Qy 356 TGTGTTATAGAGCTCAGACTCTGGACCTGCGACCTGGAATAATTTGCTACTCAGATGGTGGCTGTTT 415
Db 419 TCTCATACCGGCGGCGAGGGGTGACACGGCGGGGCACTGCGGAGAGTCTGCTGTGT 478
Qy 416 GGTATTTCTCTTCAATGACAAATGGCGCGAGTCTGATTTTAAAGTGGTACTTTTGCTC 475
Db 479 GGGTGTGGCTTCTCTGCTAGCGACCACTGCTATGCGAGTCTTCTTACAAGTCTTCTCA 538
Qy 476 GCACTAC-----AGAAATGTGAACCTGGAATTTTAAAGTGGTACTTTTGCTC 523
Db 539 GCAGCTCCATCCCGAGGGCCACTGCTATGCGAGTCTTCTTACAAGTCTTCTCA 598
Qy 524 TCCTCATCATTAATTTGGAATTCCTGATCCCACTCTTGTAGTGTCTTATTCAGCGCCC 583
Db 599 TCAGGGCTTCCACCTGGAGTCTTTTACGGCCCTTCTCTCAGCGTCACCTTCTTTAACTCA 658
Qy 584 ATATTACTGAGCGCTGTGAAGCG 608
Db 659 GCATCTACCTGAACATCCAGAGCGG 683

RESULT 14

US-09-642-852-6
; Sequence 6, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Exlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-852-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.5e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
Qy 59 TAATGTCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTCATTTTACTTTTAA 118
Db 119 TCATGGCGCTGCTCATCGTGGCCAGCGTGTGGGCAACGCGTGTCTATGCTCGCCTTCG 178
Qy 119 TTGTGGACAGAAATCTTAGACATCAAGATTAATTAATTTTCTTAACTTGGCCATTCGAG 178
Db 179 TGGCCGACTCGAGCTCGGACCCAGAACAACTTCTTCTGCTCAACCTGCGCATCTCCG 238
Qy 179 ACTTCTTTGGGTGGCAATTCGATTCCTCTGATACATCTTCTCTCGCTGAC---TTACT 235
Db 239 ACTTCTCGTGGCGCCTTCTGCACTCCACTGTATGATCCCTACGCTGCTGACAGGCGCT 298

Qy 236 GGACTTCTGGAAGCAAGCTTGTGTAATTTGGCTCAATTAAGTATCTTTTATGTACAG 295
Db 299 GGACTTCTGGCGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGAAGTACCTGCTGTGACCT 358
Qy 296 CATCTGTGTATATAATTTGCTCTCATCAGCTACGATCGCTACCAAGTCAAGTCTCAAAATGCGG 355
Db 359 CCTCTGCTTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGTCAACCGAGCGG 418
Qy 356 TGTGTTATAGAGCTCAGCACTCTGGACCTGCGACCTGGAATAATTTGCTACTCAGATGGTGGCTGTTT 415
Db 419 TCTCATACCGGCGGCGAGGGGTGACACGGCGGGGCACTGCGGAGAGTCTGCTGTGT 478
Qy 416 GGTATTTCTCTTCAATGACAAATGGCGCGAGTCTGATTTTAAAGTGGTACTTTTGCTC 475
Db 479 GGGTGTGGCTTCTCTGCTAGCGACCACTGCTATGCGAGTCTTCTTACAAGTCTTCTCA 538
Qy 476 GCACTAC-----AGAAATGTGAACCTGGAATTTTAAAGTGGTACTTTTGCTC 523
Db 539 GCAGCTCCATCCCGAGGGCCACTGCTATGCGAGTCTTCTTACAAGTCTTCTCA 598
Qy 524 TCCTCATCATTAATTTGGAATTCCTGATCCCACTCTTGTAGTGTCTTATTCAGCGCCC 583
Db 599 TCAGGGCTTCCACCTGGAGTCTTTTACGGCCCTTCTCTCAGCGTCACCTTCTTTAACTCA 658
Qy 584 ATATTACTGAGCGCTGTGAAGCG 608
Db 659 GCATCTACCTGAACATCCAGAGCGG 683

RESULT 15

US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)...(1629)
US-09-891-053-21

Query Match 9.4%; Score 110.2; DB 3; Length 2050;
Best Local Similarity 52.6%; Pred. No. 5.8e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;
Qy 59 TAATGTCTTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTCATTTTACTTTTAA 118
Db 389 TCATGGCGCTGCTCATCGTGGCCAGCGTGTGGGCAACGCGTGTCTATGCTCGCCTTCG 448
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCCATTCGAG 178

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Db 449 TGGCCGACTCGAGCTCGCACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCG 508
Qy 179 ACTTCTTTGTGGTGCATTCGAATTCCTGTATACATACCTTCTCGCTGAC---TTACT 235
Db 509 ACTTCTTGTGTCGGCGCTTCTGCAATCCCACTGTATGTATACCTAGCTGCTGACAGGCGCT 568
Qy 236 GGACTTCTGGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295
Db 569 GGACTTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACTGCTGTGCACCT 628
Qy 296 CATCTGTGTATAATATTGTCTCATACAGTACGATCGCTACAGTCTCAAAATGCCG 355
Db 629 CCTCTGCCCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCTCACCCGAGCG 688
Qy 356 TGTGGTATAGAGCTCAGCACTCTGGCACCTCGAAATTTGCTACTCAGATGGTGGCTGTTT 415
Db 689 TCTCATACCGGGCCCGACGAGGTGACACGCGCGGCGAGTCCGGAAGATGCTGCTGGTGT 748
Qy 416 GGATATTCTCTTCATGACAAATGGCGGATGATTCTGATTTTCTAGACTCTTTGGCAGAATA 475
Db 749 GGGTGTGGCCCTTCTGTGTACGACCCAGCCATCCTGAGCTGGAGTACCTGTCCGGGG 808
Qy 476 GCACCTAC-----AGAAATGTGAACCTGGATTTTAAAAAGTGGTACTTTGCTC 523
Db 809 GCAGCTCATCCCGAGGGCCACTGCTATGCGAGTTCTTCTACAACTGGTACTTCTCTCA 868
Qy 524 TCCCTACATCATATTGGAATTCCTGATCCCATCTGTTAGTTGCTTATTTTCAAGCGCC 583
Db 869 TCAGGGCTTCCACCGCTGGAGTTCCTTACGCCCTTCTCAGCGTCACTTCTTTAACTCA 928
Qy 584 ATATTACTGGAGCTGTGGAGCG 608
Db 929 GCATCTACCTGAACATCCAGAGCG 953
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OM nucleic - nucleic search, using sw model

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(without alignments)
7602.696 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDSS/ptodata/2/pubpna/US06 NEW PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07 NEW PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/US09 NEW PUB.seq.*
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- 15: /SIDSS/ptodata/2/pubpna/US60 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	270	23.1	1326	14	US-11-241-956-19
2	123	10.5	2761	11	US-11-036-196-2003
3	123	10.5	2814	14	US-11-136-527-3990
4	117.4	10.0	2824	14	US-11-136-527-127
5	72.6	6.2	2483	14	US-11-136-527-2847
6	72.4	6.2	2633	14	US-11-136-527-3114
7	71.2	6.1	1773	14	US-11-127-877-17
8	71.2	6.1	1974	14	US-11-124-368A-14
9	71	6.1	3348	11	US-11-136-527-3691
10	71	6.1	3578	11	US-11-036-196-1495
11	71	6.1	4095	14	US-11-136-527-2030
12	69.4	5.9	1401	14	US-11-127-877-4
13	68.4	5.8	2733	14	US-11-136-527-2435
14	63.8	5.5	2699	14	US-11-127-877-5
15	53.8	4.6	3741	14	US-11-136-527-751
16	53	4.5	2591	14	US-11-136-527-1944
17	52.6	4.5	2146	8	US-10-750-185-35936
18	52.6	4.5	2146	8	US-10-750-623-35936

19	51	4.4	1020	14	US-11-127-877-12	Sequence 12, Appli
20	51	4.4	1020	14	US-11-174-816-2	Sequence 2, Appli
21	51	4.4	1038	11	US-11-217-710-5	Sequence 5, Appli
22	50.6	4.3	1496	14	US-11-136-527-2608	Sequence 2608, Ap
23	49.8	4.3	85980	11	US-11-114-798-46	Sequence 46, Appli
24	49.8	4.3	197241	11	US-11-114-798-47	Sequence 47, Appli
25	49.4	4.2	1020	14	US-11-174-751-2	Sequence 2, Appli
26	45.8	3.9	1768	14	US-11-136-527-2121	Sequence 2121, Ap
27	44.8	3.8	1030	14	US-11-174-816-6	Sequence 6, Appli
28	44.8	3.8	1032	14	US-11-174-816-7	Sequence 7, Appli
29	44.8	3.8	1032	14	US-11-174-819-90	Sequence 90, Appli
30	44.8	3.8	1032	14	US-11-174-819-90	Sequence 90, Appli
31	44.8	3.8	1032	14	US-11-174-751-41	Sequence 41, Appli
32	44.8	3.8	1435	8	US-10-750-185-26145	Sequence 26145, A
33	44.8	3.8	1435	8	US-10-750-623-26145	Sequence 26145, A
34	44.2	3.8	2509	14	US-11-136-527-3738	Sequence 3738, Ap
35	43.4	3.7	1047	14	US-11-174-819-33	Sequence 33, Appli
36	42.6	3.6	1400	14	US-11-136-527-4223	Sequence 4223, Ap
37	42.6	3.6	1400	14	US-11-136-527-8086	Sequence 8086, Ap
38	41.6	3.6	1030	14	US-11-174-751-7	Sequence 7, Appli
39	41.6	3.6	1032	14	US-11-174-751-8	Sequence 8, Appli
40	41.4	3.5	1862	14	US-11-136-527-2377	Sequence 2377, Ap
41	40.2	3.4	3643	14	US-11-136-527-3725	Sequence 3725, Ap
42	40	3.4	1691140	14	US-11-091-018-1	Sequence 1, Appli
43	39.8	3.4	597	6	US-09-925-065A-573093	Sequence 573093,
44	39.8	3.4	1928	14	US-11-136-527-3095	Sequence 3095, Ap
45	39.8	3.4	2260	14	US-11-090-439-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1

US-11-241-956-19
; Sequence 19, Application US/11241956
; Publication No. US20060024792A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GRAUL Richard C.; CHAMLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
; APPLICANT: RAMKUMAR, Javalaxmi; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
; CURRENT APPLICATION NUMBER: US/11/241.956
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: US/10/398,036
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29

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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474823CB1
US-11-241-956-19

Query Match      23.1%; Score 270; DB 14; Length 1326;
Best Local Similarity 76.7%; Pred. No. 5.1e-61;
Matches 330; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 191 GTGCAATGCAATTCCTCTGTACATCTTCTCGTGAATCTTGTGAAAGC 250
Db 353 GTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTGGAAAGG 412
Qy 251 AAGCTTGTGATTTTGGCTCAATTAAGTACTGACTATCTTTATGTACAGCATCTGTGATAATA 310
Db 413 AAATCTGTGATTTTGGCTCAATTAAGTACTGACTATCTTTATGTACAGCATCTGTGATAATA 472
Qy 311 TTGTCCTCATCAGCTACGATCGCTACCAAGTCAGTCTCAAAATGCCGTGTGGTATAGAGCTC 370
Db 473 TTGTCCTCATCAGCTATGATCGATACCTGTTCAGTCTCAAAATGCTGTCTTATAGAACTC 532
Qy 371 AGCACTCGGCACCTGGAAATTCCTACTCAGATGCTGGTGGCTTTGGATATCTCCCTTCA 430
Db 533 AACATCTGGGGTCTTGAAGATTTGTTACTCTGTATGTTGGCGTGTGGGCTTCT 592
Qy 431 TGACAAATGGSCCATGATCTCGATTTTCAGACTCTTGCAGAGTACGACTACAGAAATGTG 490
Db 593 TAGTGAATGGGCCAATGATTTAGTTTCAGAGTCTTGGAAAGATGAAGTAGTGAATGTG 652
Qy 491 AACCTGGATTTTAAAAAAGTGTACTTTGCTCTCCCTACATCATATTTGGAATTCCTGA 550
Db 653 AACCTGGATTTTTCGGAATGGTATACATCTTTCGCCATCATCATCTTCTGGAATTCGTGA 712
Qy 551 TCCCATCTGTTAGTGTCTTATTTTCAGCGCCCATATTTACTGAGGCTGTGGAAAGCAG 610
Db 713 TCCCATCTGTTAGTGTCTTATTTTCAACATGAATATTTATTTGAGGCTGTGGAAAGCAG 772
Qy 611 AGAAACTGAG 620
Db 773 ATCATCTCAG 782

RESULT 2
US-11-036-196-2003
; Sequence 2003, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036.196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank Accession No. NM_053506
US-11-036-196-2003

Query Match      10.5%; Score 123; DB 11; Length 2761;
Best Local Similarity 54.0%; Pred. No. 6.3e-22;
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;

Qy 59 TAATGTCTTTACTAGCTATTGTCTATAATGTTAGGCAATGTCGTGGTCATTTTAGCTTTTA 118
Db 456 TCAATGGCGCTCTCATCGTGGCCACAGTACTGGGCAAGCGCTGGTCACTGCTCGCCTTCG 515
Qy 119 TTGTGGACAGAAATCTTTAGACATCGAAGTAATTAATCTTTTCTTAACTTGGCCATTGCGAG 178
Db 516 TGGCGGATTGCGAGCTCCGCCACCCAGAACAACTCTTTCTGTCTCAACTCGCCATCTCCG 575
Qy 179 ACTTCTTTTGGGTGCAATTTGCAATTCCTCTGTACATACCTTCTCGTCACTTAC---T 235
Db 576 ACTTCTCTGTTGGTGGCTTCTGCAATCCCATTTGACGTACCTATGCTGACCGGCGGTT 635
Qy 236 GGAATCTTGGAAAGCAAGCTTTGTGATTTTGGGCTCATTAAGTACTATCTTTTATGTACAG 295
Db 636 GGAATCTTGGCGCGGGGCTCTGCAAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 695
Qy 296 CATCTGTGTAATAATATTTCTCATCAGCTACGATCGTACCAAGTCAAGTCTCAAAATGCCG 355
Db 696 CTTGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCCTGTCACTCACTCGAGCTG 755
Qy 356 TGTGTTATAGAGCTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTT 415
Db 756 TCTCTACAGGGGCCAGAGGGGGACACAGACCGGGCGGTTCCGGAAGATGGCACTGGTGT 815
Qy 416 GGATATTTCTCTTCATGACAAATGGGCGCGATGATTTCTGATTTTCAAGACTCTTGGCAGAATA 475
Db 816 GGGTGTGGGCTTCTCTGCTGTATGGGCTGCCATCTGAGTTGGAGTACTGCTGTGGTG 875
Qy 476 GCACTACAG-----AATGTGAACCTGGATTTTAAAGTGGTACTTTGCTC 523
Db 876 GCAATTCATCCCGAGGGGCCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTTCTCA 935
Qy 524 TCCCTACATCATTTATTTGGAATTCCTGATTCGCCATCTTGTAGTCTTATTTAGCGGCC 583
Db 936 TCAGGGCTCCACCCCTCGAGTTCTTTCAGCGCCCTTCTCAGCGCTTACCTCTTCAACCTCA 995
Qy 584 ATATTTACTGGAGCTGTGGAAGCG 608
Db 996 GCATCTACCTGAACATCCAGAGGGG 1020

RESULT 3
US-11-136-527-3990
; Sequence 3990, Application US/11136527
; Publication No. US2005028750A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
```

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3990
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3990

Query Match 10.5%; Score 123; DB 14; Length 2814;
Best Local Similarity 54.0%; Pred. No. 6.3e-22;
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;
QY 59 TAAATGCTTTTACTAGCTATTGCTATAATGTTAGGCAATGTCGTGTCATTTTAGCTTTTA 118
Db 446 TCATGGCCCTGCTCATGCTGGCCACAGTACTGGGCAACGCGTGTCTATGCTCGCTTCG 505
QY 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACCTTGGCCCAATTGCAG 178
Db 506 TGGCGGATTCAGGCTCCGCCACCCAGAACACTTCTTCTGCTCAACCTCGCCATCTCG 565
QY 179 ACTTCTTTGGGTGCAATGCAATTCCTCTGTACATACCTTCTCGCTGACTTAC---T 235
Db 566 ACTTCTCTGGGTGCTCTGCTATCCCATTTGTAGTACCTTATGCTGACCGCGCGTT 625
QY 236 GGACTTCTGGAAACGACCTTGTGTAATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295
Db 626 GGACCTTTCGGCCGGGCGCTCTGCAAGCTGTGGCTGGGTAGACTTACCTACTGTGTGCT 685
QY 296 CATCTGTGTATAATTTGCTCTCATCAGTACGATGCTTACAGTCACTCTCAAATGCCG 355
Db 686 CTTGGTCTTCAACATCGTACTCATCAGTATGACCGATTCTGTGCTGCTGCTGCTGCTG 745
QY 356 TGTGGTATAGAGTCAGACCTCTGGCACCTGGAAATTTGCTACTCAGATGTCGTGCTTT 415
Db 746 TCTCTCAGGGCCAGCAGGGGGACACGAGACGGGCGCTTCGGAAGATGGCACTGGTGT 805
QY 416 GGATATTTCTCTTCATGACAAATGGCGCGATGATCTGTATTTTCAGACTTCTGGCAGATA 475
Db 806 GGGTGTGCTGCTTCTGCTGTATGGGCTGCTGATCCCTGAGTTGGGAGTACCTGTCTGTG 865
QY 476 GCACCTACAG-----AATGTGAACCTGGATTTTAAAAAAGTGGTACTTTGCTC 523
Db 866 GCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTACACTGGTACTTTCTCA 925
QY 524 TCCCTACATCATTTATGGAATTCCTGATCCCATCTTGTAGTTCCTTATTTACAGCGCCC 583
Db 926 TCACGGCTCCACCTCGAGTTCTTTCAGCGCTTCTCAGCGCTTCTCAGCGTTTACCTTCTCAACCTCA 985
QY 584 ATATTTACTGAGCTGTGGAAGCG 608
Db 986 GCATCTACTGAAATCCAGAGGCG 1010

RESULT 4
US-11-136-527-127
; Sequence 127, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127

Query Match 10.0%; Score 117.4; DB 14; Length 2824;
Best Local Similarity 50.4%; Pred. No. 1.9e-20;
Matches 285; Conservative 22; Mismatches 243; Indels 15; Gaps 2;
QY 59 TAAATGCTTTTACTAGCTATTGCTATAATGTTAGGCAATGTCGTGTCATTTTAGCTTTTA 118
Db 456 TCATGGCCCTGCTCATGCTGGCCACAGTACTGGGCAACGCGCTGTCTATGCTCGCTTCG 515
QY 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACCTTGGCCCAATTGCAG 178
Db 516 TGGCGGATTCAGGCTCCGCCACCCAGAACACTTCTTCTGCTCAACCTCGCCATCTCG 575
QY 179 ACTTCTTTGGGTGCAATTCGAATTCCTCTGTACATACCTTCTCTCGCTGACTTAC---T 235
Db 576 ACWKSSTCGTGGGTGCTTCTGCAATCCCATTTGTAGTACCTTATGCTGACCGCGCGTT 635
QY 236 GGACTTCTGGAAACGACCTTGTGTAATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295
Db 636 GGACCTTTCGGCCGGGCGCTCTGCAAGCTGTGGCTGGGTAGACTTACCTACTGTGTGCT 695
QY 296 CATCTGTGTATAATTTGCTCTCATCAGTACGATCGCTACCACTGCTCAAAATGCCG 355
Db 696 CTTGGTCTTCAACATCGTACTCATCAGTATGACCGATTCTCTGCTGCTGCTGCTGCTG 755
QY 356 TGTGGTATAGAGTCAGACCTCTGGCACCTGGAAATTTGCTACTCAGATGTCGTGCTGTTT 415
Db 756 TCTCTCAGGGCCAGCAGGGGGACACGAGACGGGCGCTTCGGAAGATGGCACTGGTGT 815
QY 416 GGATATTTCTCTTCATGACAAATGGCGCGATGATCTGTATTTTCAGACTTCTGGCAGATA 475
Db 816 GGGTGTGCTGCTTCTGCTGTATGGGCTGCTGATCCCTGAGTTGGGAGTACCTGTCTGTG 875
QY 476 GCACCTACAG-----AATGTGAACCTGGATTTTAAAAAAGTGGTACTTTGCTC 523
Db 876 GCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTACAACTGGTACTTTCTCA 935
QY 524 TCCCTACATCATTTATGGAATTCCTGATCCCATCTTGTAGTTCCTTATTTACAGCGCCC 583
Db 936 TCACGGCTCCACCTCGAGTTCTTTCAGCGCTTCTCAGCGCTTCTCAGCGTTTACCTTCTCAACCTCA 995
QY 584 ATATTTACTGAGCTGTGGAAGCG 608
Db 996 GCATCTACTGAAATCCAGAGGCG 1020

RESULT 5
US-11-136-527-2847
; Sequence 2847, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2847
; LENGTH: 2483
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2847


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; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14

Query Match          6.1%; Score 71.2; DB 14; Length 1974;
Best Local Similarity 53.4%; Pred. No. 2.8e-08;
Matches 173; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

Qy 53 CATTTTAAATGCTTTTACTAGCTATTGCTATAATGTTAGGCAATGTTGGTGTGCTGCTATTTTAG 112
Db 215 CTTCCTTAACGGGCATCTGCGCTTGTGACCATCATCGGCAATCTGGTAATTTGT 274

Qy 113 CTTTATTGTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACTTGGCCA 172
Db 275 CATTTAAGGTCAACAAGCAGCTGAAGAGCGGTCAACAACACTACTCTCTTAAGCCTGGCCT 334

Qy 173 TTGCAGACTCTTTGTGGTGCATTTGCAATTCCTCTGTACATACCTTCTCGC---TGA 229
Db 335 GTGCCGATCTGATTTATCGGGTCTATTTCAATGAATCTGTTTACGACCTACATCATCA 394

Qy 230 CTCTACTGCATCTTCGGAAGCAAGCTTGTTGATTTTGGCTCATTTACTGACTATCTTTAT 289
Db 395 ATCGATGGCCTTAGGGAACCTTGGCCTGTGTGACCTCTGCTGGCAATGACTAGTAGCCA 454

Qy 290 GTACAGCATCTGTGTATAAATTTCTCTCATCAGCTAGATCGCTACAGTCACTCTCAA 349
Db 455 GCATGCTCTGTTATGATCTTCTGTCTCATCAGCTTGTGACAGATCTTTTCCATCAGA 514

Qy 350 ATGCCGTTGTGTATAGACTCAGC 373
Db 515 GGCGCTCAGCTACCGAGCCAAAC 538

RESULT 9
US-11-136-527-3691
; Sequence 3691, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136.527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3691
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3691

Query Match          6.1%; Score 71; DB 14; Length 2348;
Best Local Similarity 53.6%; Pred. No. 3.5e-08;
Matches 171; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

Qy 53 CATTTTAAATGCTTTTACTAGCTATTGCTATAATGTTAGGCAATGTTGGTGTGCTGCTATT 112
Db 343 CCTTCCTTAACGGGCTTCTGTCATTTGTGACCATCATTTGGCAACATCTTTGTCAATG 402

Qy 113 CTTTATTGTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACTTGGCCA 172
Db 113 CTTTATTGTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACTTGGCCA 172
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Db 403 CCTTCAAGGTCAACAAACAGCTGAAGACAGTCAACAACTACTTCTCTTAAGCCTGGCCT 462
Qy 173 TTGCAGACTCTTTGTGGTGCATTTGCAATTCCTCTGTACATACCTTCTCGCTGACTT 232
Db 463 GTGCAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACTACCTACATCATATGA 522
Qy 233 AC---TGGACTTCTGGAAGCAAGCTTGTTGATTTTGGCTCATTTACTGACTATCTTTAT 289
Db 523 ACCGTTGGGCACTGGGGAACCTTAGCCTGGGACCTCTGGCTCTCCATTTGACTATGTGGCA 582
Qy 290 GTACAGCATCTGTGTATAAATTTCTCTCATCAGCTAGATCGCTACAGTCACTCTCAA 349
Db 583 GCATGCTCTGTCTCATGATCTGCTGTGCTCATCAGCTTGTGACAGTACTTTTCCATCACTA 642
Qy 350 ATGCCGTTGTGTATAGAGC 368
Db 643 GGCCACTCACCTACCGAGC 661

RESULT 10
US-11-036-196-1495
; Sequence 1495, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Blaschhoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036.196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1495
; LENGTH: 3578
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012527
US-11-036-196-1495

Query Match          6.1%; Score 71; DB 11; Length 3578;
Best Local Similarity 53.6%; Pred. No. 4.2e-08;
Matches 171; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

Qy 53 CATTTTAAATGCTTTTACTAGCTATTGCTATAATGTTAGGCAATGTTGGTGTGCTGCTATT 112
Db 252 CCTTCTTAACCTGCTTCTGTCATTTGGTGTGACCATCATTTGGCAATCTTTGTGCTGG 311
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Qy	113	CTTTTATGTGGACAGAAATCTTAGACATCGAGTAATTACTTTTTCTTAACTTGGCCA	172
Db	312	CTTTCAAGGTCAACAAACAGCTGAAGACAGTCAACAACACTACTTCTCTTAAAGCCTGGCCT	371
Qy	173	TTGCAGACTTCTTTGTGGTGCAATTGCAATTCCCTCTGTATACATCTTCCCTGGCTGACTT	232
Db	372	GTGCAGACCTGATCATCGGGGTCAITTCATGAACCTGTTCACTACCTACATCATATGA	431
Qy	233	AC---TGSACTTCTGGAAGCAAGCTGTGTGTAATTTTGGCTCATTACTGACTATCTTTTAT	289
Db	432	ACCGTTGGGCACCTGGGGAACCTTAGCTCGGACCTCTGGCTCTCCATTGACTATGTGGCCA	499
Qy	290	GTACAGCATCTGTGTATTAATTTGTCCTCATCAGCTAGACTCGCTACCAAGTCAGTCTCAA	349
Db	492	GCAATGCCCTCTGTGCATGAATCTGCTGGTTCATCAGCTTTTGACAGGTACTTTTTCCATCACTA	551
Qy	350	ATGCCGTGTGGTATAGAGC	368
Db	552	GGCCACTCACTACCGAGC	570

RESULT 11
 US-11-136-527-2030
 ; Sequence 2030, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2030
 ; LENGTH: 4095
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-2030

```

; Sequence 4, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Leenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCES: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-4

Query Match      5.9%; Score 69.4; DB 14; Length 1401;
Best Local Similarity 52.2%; Pred. No. 7.3e-08;
Matches 204; Conservative 0; Mismatches 181; Indels 6; Gaps 2;

Qy 70 CTAGCTATTGCTATATGTTAGGCAATGTCGTGGTCATTTTAGCTTTTATTGTGGACAGA 129
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 130 AATCTTAGACATCCAAAGTAAATTAATCTTTTCTTTAACTTGGCCATTCAGACTTCTTTGTG 189
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 157 CACTCCAGACCCTCAACAATTAATCTTTTATTCAGCTTGGCTGTGCTGACCTTATCAT 216
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 190 GGTGCAATTGCAATTCCTCTGTATACACCTTCCTCGCTGAC---TTACTGGACTTCTGGA 246
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 217 GGTGTTTTCCTCCATGAACCTTGTAACCCCTACACCTCTACACTGTGATGTTACTGGCCTTTGGGA 276
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 247 AAGCAAGCTTGTTGATTTTGGCTCATTAAGTACTTCTTTATGTATGATCAGCATCTGTGTAT 306
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 277 CCTGTGGTGTGACCTTTGGCTAGCCCTGGACTATGTGGTCAGCAATGCTCAGTTATG 336
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 307 AATATTGTCCTCATCAGCTACGATCGCTACCACTCTCAATGCGGTGTGTATAGA 366
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 337 AATCTGCTCATCATCAGCTTTGACAGGTACTTCTGTGTACAAAACCTCTGACCTACCCA 396
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 367 GCTCAGCAGCTCTGGCACCTGGAAAAATTTGCTACTCAGATGGTGGCTGTTCGATATCTCC 426
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 397 GTCAAGCGGAC---CACAAAATGGCAGGTATGATGATTGAGCTGGCTGGCTCTCTCT 453
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 427 TTCAATGCAAAATGGCGCGATGATTTCTGATTT 457
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 454 TTCATCCTCTGGGCTCCAGCCATTTCTTCT 484
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-11-136-527-2435
; Sequence 2435, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2435

```

LENGTH: 2733
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-2435

Query Match
Best Local Similarity 5.8%; Score 68.4; DB 14; Length 2733;
Matches 175; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 43 ATTCTTTGACATTTTAAATGCTTTTACTAGCTATTGCTATTAAGTTTAGGCAATGCTGTG 102
Db ATTACTATTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120

Qy 103 GTCAATTTAGCTTTTATTGAGACAGAAATCTTAGACATGCAAGTAAATTAATTTTCTT 162
Db GTCATGATCTCTTCAAAAGTCAACAGTCAGCTCAAGACAGTTAAACACTACTACTGCTC 1180

Qy 163 AACTTGGCCATTCAGACATCTCTTTGCTGGTGAATTTGCAATTCCTCTCTACATACCTTCC 222
Db AGCTTGGCTGTGACAGCTCATCATTTGGCATCTTCTCATGACCTCTACAGACCTAC 1240

Qy 223 TCGCTGACTTA---CTGACTTCTGGAAGCAAGCTTGTATTTTGGCTCATTAAGTAC 279
Db ATCTCTATGGAACGCTGGCTTCTGGAGTCTGGCTTGTGACCTTTGGCTGGCACTGAC 1300

Qy 280 TATCTTTTATGTACAGCATCTGTGTATTAATTTGCTTCTCATCAGCTACGATGCTAC 339
Db TATGTAGCCAGCAATGCTTCTGTCTATGAACCTTCTGGTGAATTTGATGCTTACTTT 1360

Qy 340 TCAGTCTCAAAATGCGTGTGTATAGACTCAGC 373
Db TCCATCACAGACCACTGACGTACCGGCCAAGC 1394

RESULT 14
US-11-127-877-5
Sequence 5, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merckhiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad P. P.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
PRIOR FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 2699
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-5

Query Match
Best Local Similarity 5.5%; Score 63.8; DB 14; Length 2699;
Matches 174; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

Qy 43 ATTCTTTGACATTTTAAATGCTTTTACTAGCTATTGCTATTAATTTAGGCAATGCTGTG 102
Db ATCACCATTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 464

Qy 103 GTCAATTTTGTGCTTTTATTGTCGACAGAAATCTTAGACATCGAAGTAAATTAATTTTCTT 162
Db GTCATGATCTCTTCAAGTCAACAGCCAGCTCAAGACAGTTAACACTATTAATGCTGCTC 524

Qy 163 AACTTGGCCATTCAGACATCTTTTGTGGTGAATTTGCAATTCCTCTGTGATACATCTTCC 222

Db 525 AGCTTAGCTGTGACAGATCTCATATTGGAATCTTCTCCATGAACCTCTACACCACTTAC 584
Qy 223 TCGCTGACTTA---CTGACTTCTGGAAGCAAGCTTGTGTATTTTGGCTCAATTAAGTAC 279
Db ATCTCTATGGAACGCTGGCTCTCGGAGTCTGGCTTGTGACCTTTGGCTTGCACCTGGAC 644

Qy 280 TATCTTTTATGTACAGCATCTGTGTATTAATTTGCTTCTCATCAGCTACGATGCTAC 339
Db TACGTGGCCAGCAACGCTTCTGTATGAACCTTCTGGTGAATTTTGGACCGTTACTTTT 704

Qy 340 TCAGTCTCAAAATGCGTGTGTATAGACTCAGCACTCT 378
Db TCCATCACAGACCTTGAACATATCGGCCAAGCGTACT 743

RESULT 15
US-11-136-527-751
Sequence 751, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 751
LENGTH: 3741
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-751

Query Match
Best Local Similarity 4.6%; Score 53.8; DB 14; Length 3741;
Matches 161; Conservative 9; Mismatches 166; Indels 3; Gaps 1;

Qy 93 CAATGTGCTGCTCATTTTAGCTTTTATTGTGACAGAAATCTTAGACATCGAAGTAATTA 152
Db CAACCTGTGCTGCTGTATGCGGTGTCRCACTGARGCGAAGCTACACCCGTGGGCACT 1181

Qy 153 CTTTTCCTTAACCTGGCCATTGACAGCTTCTTTGTGGGTGCAATTCGAATTCCTCTGTA 212
Db RTACATTGTGACGCTGCTGTRGCAGACCTGATTGTAGGGCAGTGTGTCATGCCCATGA 1241

Qy 213 CATAC---CTTCTCGCTGACTTACTGACCTTCTGGAAAGCAAGCTTGTGTATTTGGCT 269
Db CATCTCTATCTATCATGACACAAAGTGTCTTCTGGCGCCCTCTCTGCTCTTTGGCT 1301

Qy 270 CATTACTGACTATCTTTTATGTACAGCATCTGTGTATTAATTTGCTCATCAGCTACGA 329
Db YTCTATGATTTATGTGGCCAGCARGCATCATCTTAGTGTCTTCATCTCTGTGTATTGA 1361

Qy 330 TCGCTACCACTGACTCTCAAAATGCCGTGTGTATAGAGCTCAGCACTCTGGCACTCGAA 389
Db TCGTACCGCTCTGTCAGCAACCCCTCCGCTACTGAGGTAYCGAACCAAGACCCGKGC 1421

Qy 390 AATTGCTACTCAGATGGTGGCTGTGTTGGATTAATTCCTTT 428
Db TTCMGCTACCATCTCGGGGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1460

Search completed: April 30, 2006, 02:31:37
Job time : 628 secs

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OM protein - protein search, using sw model

Run on: April 27, 2006, 05:43:21 ; Search time 46 Seconds
(without alignments)
699.149 Million cell updates/sec

Title: US-10-626-398-10
Perfect score: 2036
Sequence: 1 MLANNSTIALTSIKISLTLFL.....LKILPVRQSTPHNRISIT 389

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/R8_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfileseq.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308.5	64.3	390	2	US-09-414-010-2
2	1308.5	64.3	390	2	US-09-812-216-2
3	1308.5	64.3	390	2	US-09-875-076-14
4	694.5	34.1	413	2	US-09-891-053-1
5	689.5	33.9	445	1	US-08-985-090-2
6	689.5	33.9	445	2	US-09-165-543-2
7	689.5	33.9	445	2	US-09-167-354-7
8	689.5	33.9	445	2	US-09-642-855-7
9	689.5	33.9	445	2	US-09-642-514-7
10	689.5	33.9	445	2	US-09-642-852-7
11	689.5	33.9	445	2	US-10-453-106-1
12	689.5	33.9	449	2	US-09-949-016-10930
13	689.5	33.9	453	2	US-09-891-053-20
14	688.5	33.8	445	2	US-10-453-106-2
15	681.5	33.5	445	2	US-09-165-543-5
16	681.5	33.5	445	2	US-09-891-053-25
17	681.5	33.5	445	2	US-10-453-106-3
18	609.5	29.9	351	2	US-09-524-162-2
19	546	26.8	362	1	US-08-985-090-5
20	546	26.8	362	2	US-09-165-543-32
21	412	20.2	355	1	US-08-118-270-11
22	412	20.2	355	4	PCT-US93-08528-11
23	410.5	20.2	348	1	US-08-118-270-13
24	410.5	20.2	348	4	PCT-US93-08528-13
25	403.5	19.8	590	2	US-09-538-092-967
26	398.5	19.6	590	2	US-09-826-509-517
27	390.5	19.2	532	2	US-09-826-509-521

28	388.5	19.1	479	1	US-08-313-553-7	Sequence 7, Appli
29	388.5	19.1	479	2	US-08-767-993-7	Sequence 7, Appli
30	385.5	18.9	429	1	US-08-748-485-7	Sequence 7, Appli
31	385.5	18.9	429	2	US-09-919-039-6	Sequence 6, Appli
32	385.5	18.9	466	1	US-08-722-001-12	Sequence 12, Appli
33	385.5	18.9	466	1	US-08-467-568-11	Sequence 11, Appli
34	385.5	18.9	466	1	US-09-030-582-11	Sequence 11, Appli
35	384.5	18.9	460	2	US-09-826-509-513	Sequence 513, App
36	384.5	18.9	466	1	US-08-406-855A-23	Sequence 23, Appli
37	384.5	18.9	466	2	US-09-206-899-23	Sequence 23, Appli
38	384.5	18.9	466	2	US-09-688-415-11	Sequence 11, Appli
39	384	18.9	466	1	US-08-334-698-6	Sequence 6, Appli
40	384	18.9	466	1	US-08-228-932-6	Sequence 6, Appli
41	384	18.9	466	1	US-08-468-933-6	Sequence 6, Appli
42	384	18.9	466	1	US-08-722-001-28	Sequence 28, Appli
43	384	18.9	466	1	US-08-406-855A-6	Sequence 6, Appli
44	384	18.9	466	1	US-08-722-190-6	Sequence 6, Appli
45	384	18.9	466	2	US-08-244-354-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monzma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414, 010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2

Query Match	64.3%	Score 1308.5;	DB 2;	Length 390;
Best Local Similarity	65.1%;	Pred. No. 3.1e-103;		
Matches	252;	Conservative	48;	Mismatches 84;
				Indels 3;
				Gaps 3;
QY	5	NSTIALT-SIKISLTLFLMSLLAIAITMLGNVVVILAFIVDRNLRHSNYFFLNLAIDPFFV	63	
Db	5	NSTINLSLSTRVTLLAFNLSLVAFLMGLNALVILAFVVDKNLRHSYFFFLNALSDPFFV	64	
QY	64	GAIAIPLYPSSLTYWTSGKQACVFWLITDYLCTASVYVNIIVLISYDRYQSVSNVAVYRA	123	
Db	65	GVISPLIPIPTLPEDWFGKEICVFWLITDYLCTASVYVNIIVLISYDRYLSVSNVAVYRT	124	
QY	124	QHSQGWKIATQWAVWIFPFMTNGPMILISDQWQNTTECEPGFLKWKYFALPTSLLLEPL	183	
Db	125	QHTGVLKIVTLWAVWVLAFLVNGPMILVSEWDEGSECEPGFSEWYLAITSFLEFV	184	
QY	184	IPILAVFYSAHYWLSLWKREKLSCLSHPLVLPSSSSSDHGHSCQDPDSRATIPARKE	243	
Db	185	IPVILVAVFNWNIYWSLWKRDHLSRCQSHPGUTA-VSSNICGHSFGRLSRSRSASSTE	243	
QY	244	TTASIGSDKSRKSLPLSIRAYKNSNVIASQWGLSHSDSLAQQRHIEIFRARKLAK	303	
Db	244	VPASPHSERQRKSLMSFSRTKNSNTIASQWGSFQSDSVALHQREHVELLRARLAK	303	
QY	304	SLAIIILAAPALCWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFLPLCHK	363	

Db 304 SLAILLGVEAVCAWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPLCHK 363

QY 364 RFQKAPLKILPVRRQSTP-PHNRIS1ST 389

Db 364 RFQKAPLKIFCIKQPLPSQHSRSVSS 390

RESULT 2

US-09-812-216-2

Sequence 2, Application US/09812216

Patent No. 6613533

GENERAL INFORMATION:

APPLICANT: Behan, Jiang Xu

APPLICANT: Hedrick, Joseph A.

APPLICANT: Laz, Thomas M.

APPLICANT: Monema, Frederick J. Jr.

APPLICANT: Morse, Kelley L.

APPLICANT: Umland, Shelby P.

APPLICANT: Wang, Suke

TITLE OF INVENTION: Histamine receptor

FILE REFERENCE: CN01069

CURRENT APPLICATION NUMBER: US/09/812,216

CURRENT FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 09/414,010

PRIOR FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

US-09-812-216-2

Query Match 64.3%; Score 1308.5; DB 2; Length 390;

Best Local Similarity 65.1%; Pred. No. 3.1e-103;

Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTALT-SIKISLTFMLSLAIAIMLGNVVILAFIVDRNLHRHSNYFFFLNLAIADFFV 63

Db 5 NSTINLSLSTRVTLAFPMFLVAFIMLGNALVILAFVVDKDLHRSSYFFFLNLAIADFFV 64

QY 64 GAIAIPLXIPSLTYWTSKQACVFWLTDYLLCTASVNIIVLISYDRYQSVSNVWYRA 123

Db 65 GVISIPLXIPHTLFEWDFGKEICVFWLTDYLLCTASVNIIVLISYDRYLSVSNVSYRT 124

QY 124 QHSGTWKIATQWAVNIWIFSMFTNGPMILSDSWQNSTTECEPGFLKWKYFALPTSLLEFL 183

Db 125 QHTGVKIVTLMVAVWVLAFLVNGPMILVSESKDEGCEPGFSEWYILAITSFLEFV 184

QY 184 IPILLVAYFAHIVYSLWKREKLSRCLSHPVLPSSDSSDHGSCRODPSRATLPARKE 243

Db 185 IPVILVAYFNMNIYSLWKRDHLRCQHPGLTA-VSSNICGHSFGRLLSRRSLASSTE 243

QY 244 TTASLGDSKRSKSLIPRAVKNSVNIASXMGFLSHSDSLAQORHIEFLFRARKLAK 303

Db 244 VPASHSEQRKRSKSLMFSRRTYKMSNTTASXMGFSQSDSVALLHQREVELLRARLAK 303

QY 304 SLAILLAAPAIWAPYSLTIVTSYFPPERNLTKSTWYHTAFWLQWNSFVNPLLYPLCHK 363

Db 304 SLAILLGVEAVCAWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPLCHK 363

QY 364 RFQKAPLKILPVRRQSTP-PHNRIS1ST 389

Db 364 RFQKAPLKIFCIKQPLPSQHSRSVSS 390

RESULT 3

US-09-875-076-14

Sequence 14, Application US/09875076

Patent No. 6869776

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Dang, Huang T.

APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/09/875,076

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,439

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,127

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,131

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/141,448

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 60/156,653

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,633

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,555

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,634

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/157,280

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,294

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,281

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,293

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,282

PRIOR FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

US-09-875-076-14

Query Match 64.3%; Score 1308.5; DB 2; Length 390;

Best Local Similarity 65.1%; Pred. No. 3.1e-103;

Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTALT-SIKISLTFMLSLAIAIMLGNVVILAFIVDRNLHRHSNYFFFLNLAIADFFV 63

Db 5 NSTINLSLSTRVTLAFPMFLVAFIMLGNALVILAFVVDKDLHRSSYFFFLNLAIADFFV 64

QY 64 GAIAIPLXIPSLTYWTSKQACVFWLTDYLLCTASVNIIVLISYDRYQSVSNVWYRA 123

Db 65 GVISIPLXIPHTLFEWDFGKEICVFWLTDYLLCTASVNIIVLISYDRYLSVSNVSYRT 124

QY 124 QHSGTWKIATQWAVNIWIFSMFTNGPMILSDSWQNSTTECEPGFLKWKYFALPTSLLEFL 183

Db 125 QHTGVKIVTLMVAVWVLAFLVNGPMILVSESKDEGCEPGFSEWYILAITSFLEFV 184

QY 184 IPILLVAYFAHIVYSLWKREKLSRCLSHPVLPSSDSSDHGSCRODPSRATLPARKE 243

Db 185 IPVLVAYFNNIYSLWDRDLHSLRCQSHPGITA-VSSNICGSHFAGRLSSRRSLASSTE 243
QY 244 TTASLGSDKRRKSLPSIRAYKSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASPHSERQRKSLSPSRRTKNSNTIASKMGFSQSDSVLHQREHVELLRRLAK 303
QY 304 SLAIIILAPAIWAPYSLTIVYSPPERNLKSTWHTAFWLOWFNSVNPFLPLCHK 363
Db 304 SLAIIILGFAVCWAPYSLTIVYSPSATGPKSVWYRTAFWLOWFNSVNPFLPLCHK 363
QY 364 RFQKAPLKILPVRRSTP-PHNRSLST 389
Db 364 RFQKAPLKILFCIKKQPLPSQHSRVSS 390

RESULT 4

US-09-891-053-1
; Sequence 1, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-891-053-1

Query Match 34.1%; Score 694.5; DB 2; Length 413;
Best Local Similarity 39.2%; Pred. No. 5.1e-51;
Matches 159; Conservative 66; Mismatches 130; Indels 51; Gaps 12;
QY 3 ANNSTIALTSIKISITFLMSLLAIAMLGNNVVILAFIVDRNLHRSNVFFLNLAIDPF 62
Db 26 ARGSAANTAV---LAALMALLIVATVIGNALVMAFVADSLRTQNFFLNLAISDFL 82
QY 63 VGAIAPLYIPSSLT-YMTSGKQACVFWLITDYLCTASVNVNIVLISYDRYOSVSNVWY 121
Db 83 VGAFCIPLVVPVLTGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSY 142
QY 122 RAQHSQGWKIAQWAVWIFSPWNGPMILISDSWQ-----NSTTE--CEPGFLKKWYPA 174
Db 143 RAQQGDTRRAVRKMLVWVLAFLYGPAIL---SWEYLSGGSSSIPEGHCAEFFYNNWYPL 199
QY 175 LPTSLEFLIPLLVAYFSAHYIWSLWKREKL---SRCLSHPLVPSDSSSS-----222
Db 200 ITASTLEFPTPLSVTFNLSIYLNIOQRTRLUGDREAGPEPPDAPSPPPAPPSCW 259
QY 223 -----DHGSHCRQDPDSRATLPARKETTASLGSKSRKSLPSIRAYKSNVIAKMG 277
Db 260 GCWPKGHEA-----MPLHSGSSSRCTERPR---SLKRGSKPSASSASLEKMK 306
QY 278 FLSHSDSLAQOREHIELFRARKLAKSLAIIILAPAIWAPYSLTIVYSPPERNLKSTWHTAFWLOWFNSVNPFLPLCHK 337

Db 307 MYSQS-----ITQR--FRLSRDKKVAKSLAIIVSIFCLCWAPYTLMLIRAAHGRCI-PD 359
QY 338 TWYHTAFWLOWFNSVNPFLYPLCHKRFQKAFKILPVRRQSTPPH 383
Db 360 WYETSFLLWANSVNPVLYPLCHYSFRRAFTKLLCPQKLVQPH 405
RESULT 5
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-2

Query Match 33.9%; Score 689.5; DB 1; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;
QY 3 ANNSTIALTSIKISITFLMSLLAIAMLGNNVVILAFIVDRNLHRSNVFFLNLAIDPF 62
Db 26 ARGSAANTAV---LAALMALLIVATVIGNALVMAFVADSLRTQNFFLNLAISDFL 82
QY 63 VGAIAPLYIPSSLT-YMTSGKQACVFWLITDYLCTASVNVNIVLISYDRYOSVSNVWY 121
Db 83 VGAFCIPLVVPVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSY 142
QY 122 RAQHSQGWKIAQWAVWIFSPWNGPMILISDSWQ-----NSTTE--CEPGFLKKWYPA 174
Db 143 RAQQGDTRRAVRKMLVWVLAFLYGPAIL---SWEYLSGGSSSIPEGHCAEFFYNNWYPL 199
QY 175 LPTSLEFLIPLLVAYFSAHYIWSLWKREKL---SRCLSHPLVPSDSSSS-----222
Db 200 ITASTLEFPTPLSVTFNLSIYLNIOQRTRLUGDREAGPEPPDAPSPPPAPPSCW 259
QY 223 -----DHGSHCRQDPDSR-----ATL-----PARKETTASLGSK 252
Db 260 GCWPKGHEAM---PLHRYGVGEAAVGAAGENTLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKSNVIAKMGFLSHSDSLAQOREHIELFRARKLAKSLAIIILAP 312

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Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSF-----QRFSLSRDRKVAKSLAVISIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPFYPLCHKRFQKAFUKI 372
Db 368 GLCWAPYTLMIIRAAAC-HGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLIKIOPHS 438

RESULT 6
US-09-165-543-2
; Sequence 2, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165.543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-165-543-2

Query Match 33.9%; Score 689.5; DB 2; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFMLSLAIAMLGNNVVILAFVDRNLHRHSYFFNLAIADFF 62
Db 26 ARGFSAAWTAV---LAALMALLIVATVGLGNALVMAFVADSSLRQTQNNFFLNLAISDFL 82
QY 63 VGAIAPIYIPSSLT-YWTSKQACVFMLITDYLCTASVNVNVLISYDRYQSYNAVWY 121
Db 83 VGAFCIPLYVPVLTGRWTFGRGLCKLWLVDDYLLCTSSAFNVLISYDRFLSVTRVSY 142
QY 122 RAQHSCTWKIATQMVAVWIFSPMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYFA 174
Db 143 RAQQGDTRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHYAEFFYNWYFL 199
QY 175 LPTSLLLEFLIPLLVAIFYSAHYWSLWKREKL-----SRCLSHVPLPSDSSS----- 222
Db 200 ITASTLEFPTPLSVTFNLSIYLNIQRRTRLRDGAREAGPEPPPPPPGCGW 259
QY 223 ----DHGHSRCQPPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSF-----QRFSLSRDRKVAKSLAVISIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPFYPLCHKRFQKAFUKI 372
Db 368 GLCWAPYTLMIIRAAAC-HGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
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QY 223 ----DHGHSRCQPPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSF-----QRFSLSRDRKVAKSLAVISIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPFYPLCHKRFQKAFUKI 372
Db 368 GLCWAPYTLMIIRAAAC-HGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLIKIOPHS 438

RESULT 7
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
; US-09-167-354-7

Query Match 33.9%; Score 689.5; DB 2; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFMLSLAIAMLGNNVVILAFVDRNLHRHSYFFNLAIADFF 62
Db 26 ARGFSAAWTAV---LAALMALLIVATVGLGNALVMAFVADSSLRQTQNNFFLNLAISDFL 82
QY 63 VGAIAPIYIPSSLT-YWTSKQACVFMLITDYLCTASVNVNVLISYDRYQSYNAVWY 121
Db 83 VGAFCIPLYVPVLTGRWTFGRGLCKLWLVDDYLLCTSSAFNVLISYDRFLSVTRVSY 142
QY 122 RAQHSCTWKIATQMVAVWIFSPMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYFA 174
Db 143 RAQQGDTRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHYAEFFYNWYFL 199
QY 175 LPTSLLLEFLIPLLVAIFYSAHYWSLWKREKL-----SRCLSHVPLPSDSSS----- 222
Db 200 ITASTLEFPTPLSVTFNLSIYLNIQRRTRLRDGAREAGPEPPPPPPGCGW 259
QY 223 ----DHGHSRCQPPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSF-----QRFSLSRDRKVAKSLAVISIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPFYPLCHKRFQKAFUKI 372
Db 368 GLCWAPYTLMIIRAAAC-HGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
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QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLKIQPHS 438

RESULT 8

US-09-642-855-7

; Sequence 7, Application US/09642855

; Patent No. 6413743

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; FILE REFERENCE: SUBTYPE

; CURRENT APPLICATION NUMBER: US/09/642,855

; CURRENT FILING DATE: 2000-08-21

; PRIOR APPLICATION NUMBER: 09/167,354

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 7

; LENGTH: 445

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE

US-09-642-855-7

Query Match 33.9%; Score 689.5; DB 2; Length 445;

Best Local Similarity 37.3%; Pred. No. 1.5e-50;

Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISITFLMSLAIAMGNVIVILAFIVDRNLHRSNYFFNLAIADFF 62

Db 26 ARGFSAATAV---LAALMALLIVATVILGNALVMLAFVADSLRTQNNFFNLAIADFF 82

QY 63 VGAIAPLYIPSSLT-YMTSGKQACVFWLITDYLLCTASVNVILISYDRVQSUSNAVY 121

Db 83 VGAFICPLYVPVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVILISYDRFLSVTRVSY 142

QY 122 RAQSGTWKIAQMVAVIFSPMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYPA 174

Db 143 RAQQDTRRAVRKMLLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFL 199

QY 175 LPTSLEFLIPIILVAYPSAHYNSLWREKL-----SRCLSHVLPSSSSS----- 222

Db 200 ITASTLEFPTPLSVTFNLSIYLNQIRTRLRLDGAAREAGPEPPPEAQPSPPPPGCW 259

QY 223 -----DHGHSCEQDPDSR-----ATL-----PARKETTASLGSDK 252

Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGATLGGGGGGSVASPTSSSGSSRGTER 316

QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRKLAKSLAILLAAP 312

Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSF-----QRFELSDRDKVAKSLAVIVSIF 367

QY 313 AICWAPYSLTVTIYSPFFERNLTSTWYHTAFWLFQNFNSFVNPFLYPLCHKRFQKAFKI 372

Db 368 GLCWAPYTLMIIRAC-HGHCVDPDYWYETSPFWLLWANSVNPVLYPLCHHSFRAPTKL 426

QY 373 LPVRRQSTPPHN 384

Db 427 LCPQKLKIQPHS 438

RESULT 9

US-09-642-514-7

; Sequence 7, Application US/09642514

; Patent No. 6437100

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; FILE REFERENCE: SUBTYPE

; CURRENT APPLICATION NUMBER: US/09/642,514

; CURRENT FILING DATE: 2000-08-21

; PRIOR APPLICATION NUMBER: US 09/167,354

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 7

; LENGTH: 445

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE

US-09-642-514-7

Query Match 33.9%; Score 689.5; DB 2; Length 445;

Best Local Similarity 37.3%; Pred. No. 1.5e-50;

Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISITFLMSLAIAMGNVIVILAFIVDRNLHRSNYFFNLAIADFF 62

Db 26 ARGFSAATAV---LAALMALLIVATVILGNALVMLAFVADSLRTQNNFFNLAIADFF 82

QY 63 VGAIAPLYIPSSLT-YMTSGKQACVFWLITDYLLCTASVNVILISYDRVQSUSNAVY 121

Db 83 VGAFICPLYVPVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVILISYDRFLSVTRVSY 142

QY 122 RAQSGTWKIAQMVAVIFSPMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYPA 174

Db 143 RAQQDTRRAVRKMLLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFL 199

QY 175 LPTSLEFLIPIILVAYPSAHYNSLWREKL-----SRCLSHVLPSSSSS----- 222

Db 200 ITASTLEFPTPLSVTFNLSIYLNQIRTRLRLDGAAREAGPEPPPEAQPSPPPPGCW 259

QY 223 -----DHGHSCEQDPDSR-----ATL-----PARKETTASLGSDK 252

Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGATLGGGGGGSVASPTSSSGSSRGTER 316

QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRKLAKSLAILLAAP 312

Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSF-----QRFELSDRDKVAKSLAVIVSIF 367

QY 313 AICWAPYSLTVTIYSPFFERNLTSTWYHTAFWLFQNFNSFVNPFLYPLCHKRFQKAFKI 372

Db 368 GLCWAPYTLMIIRAC-HGHCVDPDYWYETSPFWLLWANSVNPVLYPLCHHSFRAPTKL 426

QY 373 LPVRRQSTPPHN 384

Db 427 LCPQKLKIQPHS 438

RESULT 10

US-09-642-852-7

; Sequence 7, Application US/09642852

; Patent No. 6855560

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; FILE REFERENCE: SUBTYPE

; CURRENT APPLICATION NUMBER: US/09/642,852

; CURRENT FILING DATE: 2000-08-21

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; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7

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Query Match	33.98;	Score	689.5;	DB	2;	Length	445;
Best Local Similarity	37.3%;	Pred.	No. 1.5e-50;				
Matches	161;	Conservative	70;	Mismatches	132;	Indels	69; Gaps
							13;
QY	3	ANNSTTALT	SIKISLTFMSLLATAIMLGNNVVILAFIVDRNLRHRSNYPFNLAIADFF	62			
Db	26	ARGFSAAWTAV---	LAALMALLIVATVLGNALVMAFLAVDSSLTQNPFLLNLAISDFL	82			
QY	63	VGAIAPILYTPSSLIT-	WYTSKGKQACVFWLITDYLLCTASVNVILISYDRYQSVSNAWVY	121			
Db	83	VGAFCIPLAYPYVYL	TGRTWTGRGLCKMLVDYLLCTSSAFNVIILSYDRFLSVTRAVSY	142			
QY	122	RAGHSGTWKIATOWA	VNIWFSTFMINGPMILISDSWQ-----NSTTE--CEPGFLKKWYFA	174			
Db	143	RAOQGDTRRAVRKM	LWVLAFLYGPAII---SWEYLSGGSSTPEGHCAVFYFNWYFL	199			
QY	175	LPFTSLLEFLIPILL	VAYSAAHYWSLMWKRKL-----SRCLSHPVLPSDSSSS	222			
Db	200	ITASTLEFFPTFLSV	TPEFNLSIYLNIOQRTRLRLDGAREAAAGPPEAPSPPPPCGW	259			
QY	223	-----DHGHSRQDP	PDSCR-----ATL-----PARKETIASLSDK	252			
Db	260	GCWQKHGEAM---	PLHRYGVGEANAACAAGEATLCGGGGGGSVASPTSSSGSSSRGTER	316			
QY	253	SRRKSSLLPSIRAY	KSNVNIAASKMGFTLSHDSDLALOOREHIELFRARKLAKSLAILLAAP	312			
Db	317	PR---SLKRGSKPS	SASSASLEKRMKWVSQSF-----QRFLSRDRKVAKSIAVISIF	367			
QY	313	AICWAPYSLLTVLYS	PPFPERNLTGSTWYHTAFMWLFOWFNSFWNPPLYPLCHKRFOKAFKI	372			
Db	368	GLCWAPYLLMIIRA	C-HGHCVDDYWYEYTSFWLLWANSAVNVPVLYPLCHHSFRATFKL	426			
QY	373	LPVRRSTPPPHN	384				
Db	427	LCPOKLKIOPHS	438				

Query Match	33.9%;	Score	689.5;	DB 2;	Length	445;			
Best Local Similarity	37.3%;	Pred. No.	1.5e-50;						
Matches	161;	Conservative	70;	Mismatches	132;	Indels	69;	Gaps	13;

Qy	3	ANNSTTALTSIKISITFLMSLLAIATMGNVVVILAFIVDRNLRHESNYFEFLNLAIDPF	62
Db	26	ARGFSAANTAV---LAALMALIIVATVGNALVMLAFVADSLRTQNNFFLNLAISDFL	82
Qy	63	VGAIAIPLIPISLIT-YMTSGKQACFWMLITDYLLCTASVYNNIVLISYDROYSVSNVWY	121
Db	83	VGAFCIPLVPVYLTGRWTFGRGLCKLNLVDVYLLCTSSAFNIVLISYDRFLSVTRAVSY	142
Qy	122	RAQSGTGWKIATOMAVWIFPSFMTNGPMILISDSWQ-----NSTTE--CEPGFLKWKYPA	174
Db	143	RAQGGDTRRAVRKMLLVWVLAFLYGPAIL--SWEYLSGGSSIPSGHCVAEFPFYNNWYFL	199
Qy	175	LPSTLLEPLIPILLVAYFSAHIYWSLWKBEKL-----SRCLSHPLPSDSSS-----	222
Db	200	ITASTLEFFTPFLSVTFVFNLSIYLNIORETRLDGAAREAGPEPPPEAQSPPPPPGCGW	259
Qy	223	-----DHGHSRQDDPSR-----ATL-----PARKETTASLGSDK	252
Db	260	GCWQKGHGGRAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSSGSSSKGTER	316
Qy	253	SRKSSILLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAAF	312
Db	317	PR---SLKRGSKPSASSASLEKEMKMWOSFT-----QRPNLSRDRKVKASLAVIVSIF	367
Qy	313	AICWAPYSITVTIYSPFFPERNLTKSTWYHTAPWLQWFNFSVNNPFLYPLCHKRPQKAFIKI	372
Db	368	GLCWAFTYLLMIIRAAC-HGHCVDPDYWYETSFLLWANSVAVNPVLYPLCHHSFRRAFTKL	426
Qy	373	LPVRROSTPPHN	384
Db	427	LCPOKLKIOPHS	438

	Query Match	33.9%	Score 689.5;	DB 2;	Length 449;
	Best Local Similarity	37.3%;	Pred. No. 1.5e-50;		
	Matches 161;	Conservative 70;	Mismatches 132;	Indels 69;	Gaps 13;
Qy	3	ANNSTALTSTKISLTFLLMSLLAIATMLGNVVVILAFIVDRNLRHRSNYFFNLAIADFF	62		
Db	30	ARFGSAAWTAV---LAALMALLIVATVGNALVWLAFVADSSLRQTQNNFFLNLAISDFL	86		
Qy	63	VGAIAIPLYPISLST-YWTSGKQACVFWLITDYLLCTASVYINVLISYDRYQSVSNVWY	121		

87	Db	VGAFCIPLVYPVULVGRWTFGRGLCKLWLVDVLLCTSSAFNVILISDRFLSVTRAVSY	146
122	Qy	RAQHSQGWKTIATQMAVAVWIFSGFMTNGPMILISDSWQ-----NSTTVE--CEPGFLKKWTFA	174
147	Db	RAOQGDTRAVRKMLLVWVLAFLVGPAIL---SWEYLSGGSSIPBHCYAEFFVNYWFL	203
175	Qy	LPTSLLBFLPILILVAVPSAHYNSLWTKRL-----SRCLSHVULPSDSSSS-----	222
204	Db	ITASTLBEFFTPFLSVTFNFNLSTYILNIQRTLRLLDGAEEAGPEPPPAQSPPPPGCW	263
223	Qy	-----DGHSCSQRPDSCR-----ATL-----PARKETTASIGSDK	252
264	Db	GCWQKHGHEAM---PLHRYGVGEAAVGAEBAGETLGGGGGGGVASPTSSSGSSSRGTER	320
253	Qy	SRKSSLLPSIRAVKNNSVIAASKMGFLSHSDLSALQOREHTELPARKLAKSLAILLAAF	312
321	Db	PR---SLKRGSKPASNSASLKRKMWVSQSTF-----QRFSLSDRKVAKSLAVISIF	371
313	Qy	AICWAPYSLTTVIYSFFPPEPNRLTKSTWYHTTAPWLQWFNSFVNPFLYPLCKHRFQKAFKI	372
372	Db	GLCWAPYTLMLIIRAAC-HGHCVPDYMVYETSPFWLLWANSVNPVLYPLCHSFRAFTKL	430
373	Qy	LPVRRQSTPPHN	384
431	Db	LCPOKLIQPHS	442

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RESULT 13
US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takamura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-053-20

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[illegible]

Query Match	33.8%;	Score	688.5;	DB 2;	Length	445;			
Best Local Similarity	37.8%;	Pred. No.	1.8e-50;						
Matches	161;	Conservative	66;	Mismatches	142;	Indels	57;	Gaps	12

Qy	3	ANNSTTALTGKISLFTLMSLLAIAIMGNVVVLAIVDRNLRHRSNYFFLNLAIDPFF	62
Db	26	ARGFSAANTAV--LAALMALLIVATVLGNALVMFAFVADSSLRQTNNFFLNLAISDFL	82
Qy	63	VGAIAPIYTPSSIT-YWTSKGQACVFMLTDYLCTASVNIVLVISYDRYQSUSNAVWY	121
Db	83	VGAFCLPYYPYVLTGRWTTRGRLCKWLVDVYLCTSSAFNIVLVISYDRELSVTVAWSY	142
Qy	122	RAQSGTGWKIATOWVAWIPEFWMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYFA	174
Db	143	RAGQNTTRAVRKMLLVNVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEPFNWNIFL	199
Qy	175	LPTSLLEFLIPILLVAVFSAHYWSLMKRKL----SRCLSHPVLPSPDSSSS-----	222
Db	200	ITASTLEFPPLSVTFNFNLISIYNIQRRYRLDLDGAREAGCPPPPAEQSPPPPCCGW	259
Qy	223	-----DHGSC---RODPDSRATLPARKET-----TASIGSKK--SRRKSS	258
Db	260	GCWQKHGEAMPLHRYGVGEAAAGAEAGETALCGGGGGGSAASPSSSSSSRGTERPRS	319
Qy	259	LLPSIRAYKNKNVIASKGFELSHSDSLAQOREHIELFRARLKAKSLAILLAFAICWAP	318

Db 320 LKRGSKPSASSASLEKRMKMSQSFT-----QRFLSRDRKVAKSLAVIVSIIFGLCWAP 373
Qy 319 YSLITVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPLYPLCHKRFQKAFKILPVPRQ 378
Db 374 YTLMIIRAAC-HGHCVPDYETSFVLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKL 432
Qy 379 STPHN 384
Db 433 KIOPHS 438
RESULT 15
US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-5

Query Match 33.5%; Score 681.5; DB 2; Length 445;
Best Local Similarity 37.6%; Pred. No. 7.1e-50;
Matches 162; Conservative 65; Mismatches 135; Indels 69; Gaps 13;
Qy 3 ANNSTIALTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRSNYFFLNLAIDFF 62
Db 26 ARGFSAANTAV---LAALMALLIVATVLGNALVMAFVADSSLRTQNNFFLLNLAISDFL 82
Qy 63 VGAIAPLYIPSSLT-YWTSKQACVFWLIITDYLLCTASVYNVILISYDRYQSVSNVWY 121
Db 83 VGAFCIPLYVPVLTGRWTFGRGLKWLAVVDYLLCASSVFNLVILISYDRFSVTRAVSY 142
Qy 122 RAQSGTWKIATQMVAVIPFMTGPMILISDSWQ-----NSTTE--CEPGFLKKWYFA 174
Db 143 RAQGGDTTRAVRKMAVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHYAEFFYNWYFL 199
Qy 175 LPTSLLEFLIPLLVAFFSAHIYNSLWKREKL---SRCLSHPVLPFSDSSS----- 222
Db 200 ITASTLEFFTFPLSVTFNLSIYLNIQRRTRLRDGGREAGPEPPDAPQSPPPAPPSCW 259

Qy 223 -----DHGHSRCQDPDSR-----ATLPARKETTASLGSDK 252
Db 260 GCWPKGHGEAM---PLHRYGVGEAGPVEAGEAALGGSGGGAASPTSSSSSSSRGTGR 316
Qy 253 SRRKSSLLPSIRAYKNSNVIAASKMGFTLSHSDSLAQOREHIELFRARKLAKSLAILLA 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMSQS-----ITQR--FRLSRDKKVAKSLAIVSIF 367
Qy 313 AICWAPYSLTIVYSPFPERNLTKSTWYHTAFWLQWNSFVNPLYPLCHKRFQKAFKIL 372
Db 368 GLCWAPYTLMIIRAAACHGRCI-PDYWYETSFVLLWANSVNPVLYPLCHHSFRRAFTKL 426
Qy 373 LPVRRQSTPPH 383
Db 427 LCPQKLKVQPH 437

Search completed: April 27, 2006, 05:44:16
Job time : 47 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 27, 2006, 05:54:06 ; Search time 165 Seconds
(without alignments)
985.064 Million cell updates/sec

Title: US-10-626-398-10
Perfect score: 2036
Sequence: 1 MANNSTIALTSIKISLTLFL.....LKILPVRQSTPPHNRISIST 389

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2036	100.0	389	5	US-10-626-445-10
2	2036	100.0	389	5	US-10-626-126-10
3	2036	100.0	389	5	US-10-626-398-10
4	1308.5	64.3	390	3	US-09-812-216-2
5	1308.5	64.3	390	3	US-09-910-411-2
6	1308.5	64.3	390	3	US-09-875-076-14
7	1308.5	64.3	390	3	US-09-876-252-14
8	1308.5	64.3	390	3	US-09-852-165-2
9	1308.5	64.3	390	3	US-09-891-138A-6
10	1308.5	64.3	390	4	US-10-052-193-2
11	1308.5	64.3	390	4	US-10-225-567A-629
12	1308.5	64.3	390	4	US-10-272-983-14
13	1308.5	64.3	390	4	US-10-354-769-2
14	1308.5	64.3	390	4	US-10-393-807-14
15	1308.5	64.3	390	4	US-10-417-820A-14
16	1308.5	64.3	390	4	US-10-349-253A-2
17	1308.5	64.3	390	4	US-10-696-673-2
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19	1308.5	64.3	390	4	US-10-782-596-14
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21	1308.5	64.3	390	5	US-10-626-445-10
22	1308.5	64.3	390	5	US-10-684-206-20
23	1308.5	64.3	390	5	US-10-616-088-2
24	1308.5	64.3	390	5	US-10-626-126-2
25	1308.5	64.3	390	5	US-10-626-398-2
26	1308.5	64.3	390	5	US-10-756-149-4702
27	1308.5	64.3	390	5	US-10-723-955-14

28	1308.5	64.3	390	5	US-10-488-421-8	Sequence 8, Appli
29	1306.5	64.2	390	4	US-10-290-078-27	Sequence 27, Appli
30	1306.5	64.2	390	5	US-10-488-421-6	Sequence 6, Appli
31	1237	60.8	391	5	US-10-626-445-8	Sequence 8, Appli
32	1237	60.8	391	5	US-10-626-126-8	Sequence 8, Appli
33	1237	60.8	391	5	US-10-626-398-8	Sequence 8, Appli
34	1236.5	60.7	391	5	US-10-626-445-9	Sequence 9, Appli
35	1236.5	60.7	391	5	US-10-626-126-9	Sequence 9, Appli
36	1236.5	60.7	391	5	US-10-626-398-9	Sequence 9, Appli
37	1166	57.3	357	5	US-10-488-421-4	Sequence 4, Appli
38	1048.5	51.5	336	5	US-10-488-421-2	Sequence 2, Appli
39	694.5	34.1	413	3	US-09-891-053-1	Sequence 1, Appli
40	694.5	34.1	413	5	US-10-759-463-1	Sequence 1, Appli
41	689.5	33.9	445	3	US-09-350-206-2	Sequence 2, Appli
42	689.5	33.9	445	3	US-09-349-755-2	Sequence 2, Appli
43	689.5	33.9	445	3	US-09-166-334-2	Sequence 2, Appli
44	689.5	33.9	445	4	US-10-282-958-2	Sequence 2, Appli
45	689.5	33.9	445	4	US-10-225-567A-549	Sequence 549, App

ALIGNMENTS

RESULT 1
US-10-626-445-10
; Sequence 10, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-445-10

Query Match	100.0%	Score 2036;	DB 5;	Length 389;
Best Local Similarity	100.0%;	Pred. No. 7.6e-170;		
Matches 389;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MANNSTIALTSIKISLTLFLMSLLAIAIMLGNVVVILAFIVDRNLHRNSYFFLNLAIAD	60	
Db	1	MANNSTIALTSIKISLTLFLMSLLAIAIMLGNVVVILAFIVDRNLHRNSYFFLNLAIAD	60	
QY	61	FPVGAIAIPLYIPSSLTWTSGKQACVFWLIITDYLLCTASVNVILISYDRQSVSNVW	120	
Db	61	FPVGAIAIPLYIPSSLTWTSGKQACVFWLIITDYLLCTASVNVILISYDRQSVSNVW	120	
QY	121	YRAQHSIGTWKIATQVAVWIFSMFTNGPMILISDSQNSSTTECEPGFLKKYFALPTSLL	180	
Db	121	YRAQHSIGTWKIATQVAVWIFSMFTNGPMILISDSQNSSTTECEPGFLKKYFALPTSLL	180	
QY	181	EPLIPILVAYPSAHYWSLWKREKLSRCLSHPVLPSSSSSDHGHSCRDQPSRATLPA	240	
Db	181	EPLIPILVAYPSAHYWSLWKREKLSRCLSHPVLPSSSSSDHGHSCRDQPSRATLPA	240	
QY	241	RKETTASIGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLALQOREHIELFRANK	300	
Db	241	RKETTASIGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLALQOREHIELFRANK	300	
QY	301	LAKSLAILLAAPAI CWAPYSLTTVIYSFPFPERNLTKSTWYHTAFWLQWFNSFVNPFLYPL	360	
Db	301	LAKSLAILLAAPAI CWAPYSLTTVIYSFPFPERNLTKSTWYHTAFWLQWFNSFVNPFLYPL	360	

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QY 361 CHKRFQKAFKILPVRROSTPPHNRISST 389
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Db 361 CHKRFQKAFKILPVRROSTPPHNRISST 389
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RESULT 2
US-10-626-126-10
; Sequence 10, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-126-10

Query Match 100.0%; Score 2036; DB 5; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.6e-170;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNSTIALTSIKISLTFLMSLLAIAMLGNNVVILAFIVDRNLHRHSNFFFLNLAIAD 60
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Db 1 MANNSTIALTSIKISLTFLMSLLAIAMLGNNVVILAFIVDRNLHRHSNFFFLNLAIAD 60
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QY 61 PFVGAIAIPLYPSSLTWTSGKQACVFLLITDYLLCTASVNVIVLISYDRYQSVNAW 120
|||||
Db 61 PFVGAIAIPLYPSSLTWTSGKQACVFLLITDYLLCTASVNVIVLISYDRYQSVNAW 120
|||||
QY 121 YRAQSGTWKIATQMAVWIFSPMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
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Db 121 YRAQSGTWKIATQMAVWIFSPMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
|||||
QY 181 EFLPIILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHSCQDPDSRATLPA 240
|||||
Db 181 EFLPIILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHSCQDPDSRATLPA 240
|||||
QY 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARK 300
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Db 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARK 300
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QY 301 LAKSLAILLAFAICWAPYSLTVIYSPFPERNLTKSTWYHTAFWLQWFNSFVNPFYPL 360
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Db 301 LAKSLAILLAFAICWAPYSLTVIYSPFPERNLTKSTWYHTAFWLQWFNSFVNPFYPL 360
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Db 361 CHKRFQKAFKILPVRROSTPPHNRISST 389
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RESULT 3
US-10-626-398-10
; Sequence 10, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
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; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-398-10

Query Match 100.0%; Score 2036; DB 5; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.6e-170;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNSTIALTSIKISLTFLMSLLAIAMLGNNVVILAFIVDRNLHRHSNFFFLNLAIAD 60
|||||
Db 1 MANNSTIALTSIKISLTFLMSLLAIAMLGNNVVILAFIVDRNLHRHSNFFFLNLAIAD 60
|||||
QY 61 PFVGAIAIPLYPSSLTWTSGKQACVFLLITDYLLCTASVNVIVLISYDRYQSVNAW 120
|||||
Db 61 PFVGAIAIPLYPSSLTWTSGKQACVFLLITDYLLCTASVNVIVLISYDRYQSVNAW 120
|||||
QY 121 YRAQSGTWKIATQMAVWIFSPMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
|||||
Db 121 YRAQSGTWKIATQMAVWIFSPMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
|||||
QY 181 EFLPIILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHSCQDPDSRATLPA 240
|||||
Db 181 EFLPIILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHSCQDPDSRATLPA 240
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QY 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARK 300
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Db 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARK 300
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QY 301 LAKSLAILLAFAICWAPYSLTVIYSPFPERNLTKSTWYHTAFWLQWFNSFVNPFYPL 360
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Db 301 LAKSLAILLAFAICWAPYSLTVIYSPFPERNLTKSTWYHTAFWLQWFNSFVNPFYPL 360
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QY 361 CHKRFQKAFKILPVRROSTPPHNRISST 389
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Db 361 CHKRFQKAFKILPVRROSTPPHNRISST 389
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RESULT 4
US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
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Matches	252;	Conservative	48;	Mismatches	84;	Indels	3;	Gaps	37;
QY	5	NSTIALT-SIKISLTFMLSLAIAIMLGNVNVILAFIVDRNLHRSSVFFNLAIADPFV	63						
Db	5	NSTINLSLSTRTVTLAFPMSLVAPAIMLGNALVILAFVVDKNLHRSSVFFNLAIADPFV	64						
QY	64	GAIAIPLYIPSSLTWTYSGKQACVFMLITDYLCTASVYNILVLSIDRYQSVNAVMYRA	123						
Db	65	GVISIPLYIPHTLFEWDFGKEICVFMLTDDYLCTASVYNILVLSIDRYLSVNAVSRT	124						
QY	124	QHGSTWKIATQMAVWITPSPMTNGPMILISDSQNSTTECEPGFLKKWYFALPTSLLEFL	183						
Db	125	QHTGVLKIVTLMAVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYILAITSLFEV	184						
QY	184	IPILLVAYFAHYYWSLWKEKLSRCLSHPVLPDSDDSSDHGHSRQDDPSRATLPARKE	243						
Db	185	IPVILVAYFMNYYWSLWKRDHLRCKSQSHPGTLA-VSSNICGHSFRGRLSSRRSLASTE	243						
QY	244	TTASLGDGSKRRKSSLLPSTRAYKGNVIVASKMGFLSHSDSLAQOREHIELFRARKLAK	303						
Db	244	VPASFHSERQRRKSSLMFFSRTKMNSTIASKMGSPQSQSDVALHQREHVELLRARLAK	303						
QY	304	SLAILLAAPALCWAPYSLTTVTIVISFFPERNLTKTWTHTAFWLQWPNFSVFNPLYPLCHK	363						
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QY	364	RFQAKFLKILPVRRQSTP-PHNRISIT	389						
Db	364	RFQAKFLKIFCIKKOPLPFSOHSRSRVSS	390						

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RESULT 5
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

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Query Match	64.3%	Score 1308.5;	DB 3;	Length 390;
Best Local Similarity	65.1%;	Pred. No. 4.6e-106;		
Matches 252; Conservative	48;	Mismatches 84;	Indels 3;	Gaps 3;

QY	5	NSTIALT-STKISLTFMLSLAIAIMLGNNVVILAFIVDRNLRRHSNYFFTLNLAIDPFV	63
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Db	5	NSIINLSLSTRVTLFAFMSLVAPAIMGLNALVILAFVVDKNLRHRSYFFTLNLAISDPFV	64
		: : : : :	
QY	64	GAIAIPYIPSSLTYFTSGKOACVFMLITDYLLCTASVYNIVLTSYDYSQSVSNAWTRA	123
		: : :	
Db	65	GVISIPLYIPTHLFEWDFGKEICVFMLTTDYLLCTASVYNIVLTSYDRLSVSNAVSVRT	124
		: : :	
QY	124	QHSGTWKVIATOMVAWITFSRWNTGMILISDSWQNSTTECBPGFLKKWFALPTSLLEPL	183
		: : : : :	

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Db      125 QHTGVKIVTLVMAVWVLAFLVNGPMILVSSWKDGESECEPGFSEWVILAITSPLETV 181
Qy      184 IPILLVAYFSAHIYWSLWKREKLSCHLPVLPDSSSDSGHSCRDQDPDSRATLPARKE 243
Db      185 IPVLVAYFNNNIYWSLWKRDHLSCQSHPG/LTA-VSSNICGHSFPRGLSSRRSLASASTE 243
Qy      244 TTASLGDKSRKSKSLPSIRAYKNSNVIASKMGFLSHSDSLALOORHIEFLPRARKLAK 303
Db      244 VPASFHSERQRRKSLPSSSTKWNSTIASKMGSFQSQSDSVLHQREHVELLRARLAK 303
Qy      304 SLAIIILAAFAICWAPYSLTIIYVYISFFPBRNLTKSTWYHTAFWLQWFNSFVNPFYPLCHK 363
Db      304 SLAIIILGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPFYPLCHK 363
Qy      364 RFQAKFLKILPVRROSTP-PHNRISIT 389
Db      364 RFQAKFLKIFCICKQPLPQSHRSVSS 390

RESULT 6
US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: ASEN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282

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; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match      64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

Qy 5 NSTALT-SIKISITFLMSLLAIAIMLGNNVVILAFIVDRNLHRSNYFFLNLAIDFFV 63
Db 5 NSTINLSLSTRTVTLAFPFMSLVAFALMGLNALVILAFVVDKNNLRSSYFFLNLAISDFFV 64

Qy 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVAVYRA 123
Db 65 GVISIPLYIPHTLFEWDFGKEICVFWLTDTYLLCTASVYNIIVLSYDRYLSVSNVAVSYRT 124

Qy 124 QHSGTWKIATQMWAVWIFSPFMTNGPMILISDSWQNSTTECPGFLKKWYFALPTSLLLEFL 183
Db 125 QHTGVKIVTLMWAVWLAFVNGPMILVSESWKDEGSECEPGFSEWYILAITSFLEFV 184

Qy 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCRODPPDSRATLPARKE 243
Db 185 IPVLIVAFYFNWNIYWSLWKRDHLSCQSHPGGLTA-VSSNICGHSFRGLSSRRSLASTE 243

Qy 244 TTSILGSDKSRKSLIPSIKAYKNSNVIAASKMGFLSHSDSLAQOREHIELFARKLAK 303
Db 244 VPASFHSERQQRKSLSPSSSTKNSNTIASKMGSPSQSDSVLHQREHVELLRARLAK 303

Qy 304 SLAILLAFAICWAPYSITTVIYGFPPERNITKSTWHTAFWLQWFSNVNPFYPLCHK 363
Db 304 SLAILLGVAFCWAPYSITFTVLFSYSSATGPKSVYRIAFWLQWFSNVNPFYPLCHK 363

Qy 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKIFCIKKQPLPSQHSRVS 390

RESULT 7
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liew, Chen W
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match      64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

Qy 5 NSTALT-SIKISITFLMSLLAIAIMLGNNVVILAFIVDRNLHRSNYFFLNLAIDFFV 63
Db 5 NSTINLSLSTRTVTLAFPFMSLVAFALMGLNALVILAFVVDKNNLRSSYFFLNLAISDFFV 64

Qy 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVAVYRA 123
Db 65 GVISIPLYIPHTLFEWDFGKEICVFWLTDTYLLCTASVYNIIVLSYDRYLSVSNVAVSYRT 124

Qy 124 QHSGTWKIATQMWAVWIFSPFMTNGPMILISDSWQNSTTECPGFLKKWYFALPTSLLLEFL 183
Db 125 QHTGVKIVTLMWAVWLAFVNGPMILVSESWKDEGSECEPGFSEWYILAITSFLEFV 184

Qy 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCRODPPDSRATLPARKE 243
Db 185 IPVLIVAFYFNWNIYWSLWKRDHLSCQSHPGGLTA-VSSNICGHSFRGLSSRRSLASTE 243
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QY 244 TTASLGSKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLQREHVELLRARRLAK 303
QY 304 SLAIIAFAICWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFYPLCHK 363
Db 304 SLAIIIGFVAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKILPVRRQSTP-PHNRISIT 389

RESULT 8
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind Peter
; APPLICANT: Sejitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1el G Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-852-165-2

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNNVVILAFIVDRNLHRHSYFFFLNLAIADPFV 63
Db 5 NSTINLSLSTRVTLAFPMFLVAFIMLGNALVILAFVVDKRLHRSSYFFFLNLAIADPFV 64
QY 64 GAIAIPLYPSSLTYTSGKQACVFWLITDYLCTASVNVNVLISYDRYSQSVNAWYRA 123
Db 65 GVISIPLYIPTLFEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYSQSVNAWYRA 124
QY 124 QHSGTWKIATQWAVWIFSPMTNGPMILISDQWNSSTCEPGFLKKWYFALPTSLLEPL 183
Db 125 QHTGVLTIVTLVAVWVLAFLVNGPMILVSVSKDEGCECPGFSEWYILAITSFLEFV 184
QY 184 IPIILVAFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCQDPDSTRATUPARKE 243
Db 185 IPVILVAYFNNIYWSLWKRDHLSCQSHPLGTA-VSSNICGHSFGRSLSRSSLSASTE 243
QY 244 TTASLGSKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLQREHVELLRARRLAK 303
QY 304 SLAIIAFAICWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFYPLCHK 363
Db 304 SLAIIIGFVAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKILPVRRQSTP-PHNRISIT 389

RESULT 9
US-09-891-138A-6
; Sequence 6, Application US/09891138A
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; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
; US-09-891-138A-6

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNNVVILAFIVDRNLHRHSYFFFLNLAIADPFV 63
Db 5 NSTINLSLSTRVTLAFPMFLVAFIMLGNALVILAFVVDKRLHRSSYFFFLNLAIADPFV 64
QY 64 GAIAIPLYPSSLTYTSGKQACVFWLITDYLCTASVNVNVLISYDRYSQSVNAWYRA 123
Db 65 GVISIPLYIPTLFEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYSQSVNAWYRA 124
QY 124 QHSGTWKIATQWAVWIFSPMTNGPMILISDQWNSSTCEPGFLKKWYFALPTSLLEPL 183
Db 125 QHTGVLTIVTLVAVWVLAFLVNGPMILVSVSKDEGCECPGFSEWYILAITSFLEFV 184
QY 184 IPIILVAFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCQDPDSTRATUPARKE 243
Db 185 IPVILVAYFNNIYWSLWKRDHLSCQSHPLGTA-VSSNICGHSFGRSLSRSSLSASTE 243
QY 244 TTASLGSKSRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLQREHVELLRARRLAK 303
QY 304 SLAIIAFAICWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFYPLCHK 363
Db 304 SLAIIIGFVAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKILPVRRQSTP-PHNRISIT 389

RESULT 10
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
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ORGANISM: Homo sapiens
US-10-052-193-2

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTALT-SIKISLFLMSLAIAMLGNNVVLAFIVDRNLRHRSNYFFFLNLAIDPFV 63
DB 5 NSTINLSLSTRVTLAFVMSLAFALMGLNALVILAFVVDKMLRHRSSYFFFLNLAISDFV 64

QY 64 GAIAIPLYPSSLTYWTSGKQACVFWLITDYLCTASVNVILISYDRYQSVNAVWYRA 123
DB 65 GVISIPLYPHTLPEWDFGKEICVFWLITDYLCTASVNVILISYDRYQSVNAVYRT 124

QY 124 QHSGTWKIATQWAVWIFSPMTNGPMILISQWNSQNTTECEPGFKKQWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLWVAVVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYIILAITSFLEFV 184

QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCRODPPDSRATLPARK 243
DB 185 IPVILVAFNNIYWSLWKRDHLSCQHPGLTA-VSSNICGHSFGRGLSRRSLASTE 243

QY 244 TTASIGSKRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAK 303
DB 244 VPASFHSEQRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRARLAK 303

QY 304 SLAILLAFAICWAPYSLTTVIYSPFFERNLTGSTWHTAFWLFQWFNFSVNPFLYPLCHK 363
DB 304 SLAILLGVFAVCWAPYSLTIVLSFYSSATGPKSVWYRIAFWLFQWFNFSVNPFLYPLCHK 363

QY 364 RFQKAFKILPVRRQSTP-PHNRSIST 389
DB 364 RFQKAFKILFCIKKQPLPSQHSRSVSS 390

RESULT 11
US-10-225-567A-629
Sequence 629, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patent In version 3.1
SEQ ID NO 629
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTALT-SIKISLFLMSLAIAMLGNNVVLAFIVDRNLRHRSNYFFFLNLAIDPFV 63
DB 5 NSTINLSLSTRVTLAFVMSLAFALMGLNALVILAFVVDKMLRHRSSYFFFLNLAISDFV 64

QY 64 GAIAIPLYPSSLTYWTSGKQACVFWLITDYLCTASVNVILISYDRYQSVNAVWYRA 123
DB 65 GVISIPLYPHTLPEWDFGKEICVFWLITDYLCTASVNVILISYDRYQSVNAVYRT 124

QY 124 QHSGTWKIATQWAVWIFSPMTNGPMILISQWNSQNTTECEPGFKKQWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLWVAVVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYIILAITSFLEFV 184

Db 125 QHTGVLKIVTLWVAVVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYIILAITSFLEFV 184

QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCRODPPDSRATLPARK 243
Db 185 IPVILVAFNNIYWSLWKRDHLSCQHPGLTA-VSSNICGHSFGRGLSRRSLASTE 243

QY 244 TTASIGSKRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASFHSEQRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRARLAK 303

QY 304 SLAILLAFAICWAPYSLTTVIYSPFFERNLTGSTWHTAFWLFQWFNFSVNPFLYPLCHK 363
Db 304 SLAILLGVFAVCWAPYSLTIVLSFYSSATGPKSVWYRIAFWLFQWFNFSVNPFLYPLCHK 363

QY 364 RFQKAFKILPVRRQSTP-PHNRSIST 389
Db 364 RFQKAFKILFCIKKQPLPSQHSRSVSS 390

RESULT 12
US-10-272-983-14
Sequence 14, Application US/10272983
Publication No. US20030148450A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-983-14

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTALT-SIKISLFLMSLAIAMLGNNVVLAFIVDRNLRHRSNYFFFLNLAIDPFV 63
DB 5 NSTINLSLSTRVTLAFVMSLAFALMGLNALVILAFVVDKMLRHRSSYFFFLNLAISDFV 64

QY 64 GAIAIPLYPSSLTYWTSGKQACVFWLITDYLCTASVNVILISYDRYQSVNAVWYRA 123
DB 65 GVISIPLYPHTLPEWDFGKEICVFWLITDYLCTASVNVILISYDRYQSVNAVYRT 124

QY 124 OHSGTWKIATQWAVWIFPMFTNGPMILSDSQWSTTECEPGFLKKWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLMAVWVLAFLVNGPMILVSESKWDEGSECEPGFSEWILAITSPLEFV 184
QY 184 IPILLVAYPSAHYIYSLWREKLSRCLSHPVLPSPSSSDHGHSCRODPSRATLPARKE 243
DB 185 IPVILVAYFNMNIYSLWLRDHLRCQSHPGTLA-VSSNICGHSFRGLSSRRSLASAE 243
QY 244 TTASLGSDKSRKSSLLPSIRAYKSNVTASKMGFLSHSDSLALQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSLMPFSRRTKMSNTTASKMGSPSQSDSVLHQREHVELLRARLAK 303
QY 304 SLAIIILAAFAICWAPYSLTIVYSPFERNLTSTWYHTAFWLQWNSFVNPFYPLCHK 363
DB 304 SLAIIILGVFAVCWAPYSLTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFYPLCHK 363
QY 364 RFQKAFKLKILPVRRQSTP-PHNRISST 389
DB 364 RFQKAFKLKIFCIKKQPLPSQHSRSVSS 390

RESULT 13

US-10-354-769-2
; Sequence 2, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-769-2

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKSLTFLMSLAIATMLGNVVILAFIVDRNLRHSNVEFFNLATADPFV 63
DB 5 NSTINLSLSTRVTLAFPMFLSLVAFIMLGNALVILAFVVDKNRHRSYFFFLNLAISDFPV 64
QY 64 GAIAIPLYIPSSLTWYTSKQACVFWLITDYLCTASVYNIIVLISYDRYQSVSNVWYRA 123
DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVYNIIVLISYDRVLSVSNVSYRT 124
QY 124 QHSGTWKIATQWAVWIFPMFTNGPMILSDSQWSTTECEPGFLKKWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLMAVWVLAFLVNGPMILVSESKWDEGSECEPGFSEWILAITSPLEFV 184
QY 184 IPILLVAYPSAHYIYSLWREKLSRCLSHPVLPSPSSSDHGHSCRODPSRATLPARKE 243
DB 185 IPVILVAYFNMNIYSLWLRDHLRCQSHPGTLA-VSSNICGHSFRGLSSRRSLASAE 243
QY 244 TTASLGSDKSRKSSLLPSIRAYKSNVTASKMGFLSHSDSLALQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSLMPFSRRTKMSNTTASKMGSPSQSDSVLHQREHVELLRARLAK 303

QY 304 SLAIIILAAFAICWAPYSLTIVYSPFERNLTSTWYHTAFWLQWNSFVNPFYPLCHK 363
DB 304 SLAIIILGVFAVCWAPYSLTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFYPLCHK 363
QY 364 RFQKAFKLKILPVRRQSTP-PHNRISST 389
DB 364 RFQKAFKLKIFCIKKQPLPSQHSRSVSS 390

RESULT 14

US-10-393-807-14
; Sequence 14, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-14

Query Match 64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKSLTFLMSLAIATMLGNVVILAFIVDRNLRHSNVEFFNLATADPFV 63
DB 5 NSTINLSLSTRVTLAFPMFLSLVAFIMLGNALVILAFVVDKNRHRSYFFFLNLAISDFPV 64
QY 64 GAIAIPLYIPSSLTWYTSKQACVFWLITDYLCTASVYNIIVLISYDRYQSVSNVWYRA 123
DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVYNIIVLISYDRVLSVSNVSYRT 124
QY 124 QHSGTWKIATQWAVWIFPMFTNGPMILSDSQWSTTECEPGFLKKWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLMAVWVLAFLVNGPMILVSESKWDEGSECEPGFSEWILAITSPLEFV 184
QY 184 IPILLVAYPSAHYIYSLWREKLSRCLSHPVLPSPSSSDHGHSCRODPSRATLPARKE 243
DB 185 IPVILVAYFNMNIYSLWLRDHLRCQSHPGTLA-VSSNICGHSFRGLSSRRSLASAE 243
QY 244 TTASLGSDKSRKSSLLPSIRAYKSNVTASKMGFLSHSDSLALQOREHIELFRARKLAK 303

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 27, 2006, 05:55:16 ; Search time 26 Seconds
(without alignments)
680.419 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	689.5	33.9	445	7	US-11-115-564-1 Sequence 1, Appli
2	688.5	33.8	445	7	US-11-115-564-2 Sequence 2, Appli
3	681.5	33.5	445	7	US-11-115-564-3 Sequence 3, Appli
4	549	27.0	441	7	US-11-241-956-3 Sequence 3, Appli
5	403.5	19.8	590	7	US-11-124-368A-183 Sequence 183, App
6	403.5	19.8	590	7	US-11-127-877-54 Sequence 54, Appl
7	395.5	19.4	532	7	US-11-127-877-42 Sequence 42, Appl
8	386.5	19.0	487	7	US-11-249-847-582 Sequence 582, App
9	385.5	18.9	429	7	US-11-127-877-51 Sequence 51, Appl
10	385.5	18.9	466	7	US-11-127-877-50 Sequence 50, Appl
11	373	18.3	466	7	US-11-127-877-41 Sequence 41, Appl
12	370	18.2	400	6	US-10-499-210-2 Sequence 2, Appli
13	356.5	17.5	353	6	US-10-875-716-10 Sequence 10, Appl
14	340.5	16.7	350	7	US-11-165-024-3 Sequence 3, Appli
15	338	16.6	458	7	US-11-232-805-46 Sequence 46, Appl
16	338	16.6	480	6	US-10-521-162-40 Sequence 40, Appl
17	336	16.5	462	7	US-11-232-805-44 Sequence 44, Appl
18	322.5	15.8	450	7	US-11-232-805-26 Sequence 26, Appl
19	322.5	15.8	450	7	US-11-232-805-27 Sequence 27, Appl
20	314.5	15.4	447	7	US-11-232-805-8 Sequence 8, Appli
21	313	15.4	450	7	US-11-232-805-7 Sequence 7, Appli
22	304	14.9	458	6	US-10-877-346-51 Sequence 51, Appl
23	296.5	14.6	475	6	US-10-877-346-48 Sequence 48, Appl
24	294	14.4	446	7	US-11-166-412-67 Sequence 67, Appl
25	292.5	14.4	365	6	US-11-875-716-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-11-115-564-1
; Sequence 1, Application US/11115564
; Publication No. US20050267116A1
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlwes, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-a]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-a]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-a]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/11/115,564
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-115-564-1

Query Match	33.9%	Score	689.5;	DB	7;	Length	445;
Best Local Similarity	37.3%	Pred. No.	1.4e-54;				
Matches	161;	Conservative	70;	Mismatches	132;	Indels	69;
Gaps	13;						
QY	3	ANNSTIALTSIKISITFLMSLLAIIMLGWVVILAFIVDRNLHRSNVFFLNLAIDPF	62				
DB	26	ARGSAATAV---LAALMALLIVATVGNALWMLAFVADSLRTQNNFFLNLAISDFL	82				
QY	63	VGAITAIPYIPSSLT-YMTSGKQACVFWLITDYLCTASVYVNIIVLISYDRYQSVNAVWY	121				
DB	83	VGAFICPIYVPVLTGRTFTGRLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRVSY	142				
QY	122	RAQHSQTKIATQWVAVMIFSPMTNGPMLISDSMQ-----NSTTE--CEPGFLKKWYPA	174				
DB	143	RAQQGDTTRAVRKMVLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCAEFYNNWYFL	199				
QY	175	LPTSLLEFLIPLLVAFYSAHYWSLWREKL-----SRCLSHPVLPSSSSS-----	222				
DB	200	ITASTLEFPTPLSVTFNLSIYLNIOQRTLRLLDGNAREAGPEPPPPPPGPGCW	259				
QY	223	-----DHGHSRCQDDPSR-----ATL-----PARKETTASIGSDK	252				
DB	260	GCWQKHGEAM---PLHRYGVGEAAVGAAGENTLGGGGGGSVASPTSSSSSSSRGTER	316				


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; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 582
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-249-847-582

Query Match      19.0%; Score 386.5; DB 7; Length 487;
Best Local Similarity 23.2%; Pred. No. 3.9e-27;
Matches 114; Conservative 85; Mismatches 158; Indels 135; Gaps 14;

QY      1  MLANNSTIALTSIKISITELMSLAIAMILGNVVVILAFIDRNLRHSNVFPLNLAID 60
DB      14  MCEGNKTMASPOLMPLVVLVLTICLVTVGLNLLVLYAVRSERKLTHTVGNLYVLSLVD 73

QY      61  FFGAIAIP---LYIPSSLTWTSGKQACVFWLITDYLLCTASVYINVLISYDIYQSVSN 117
DB      74  LIVGAVVPMNIIYL---LMSKWSLGRPLCLFWLSMDIVASTASIFSIFILCIDYRSVQQ 131

QY      118  AVMYRAQHSQTKIATQMAVWIPSPFWTNGPMILISDSQNSTT---ECEPGLKKWYF 173
DB      132  PLRYLKVRTKTRASAT-ILGAWPLSLFWLWIPILGNHFMQOTSVRREDKCEITDFYDVTWF 190

QY      174  ALPTSLLEFLIPILLVAFSAHIY-----KLSRCLSHPYL----- 197
DB      191  KVMTAIINFYPLTLLMLWFYAKIYKAVRQCHRELINRSLPSFSEIKLRPENPKGDAXK 250

QY      198  -----WSLWKRE-----KLSRCLSHPYL----- 215
DB      251  PGKESPEVWLUKRPKDGAGGSVLKSPQTPKEMKSPVVFSGQEDREVDKLYCPPLDIVHM 310

QY      216  --PSDSSSD-----HGHS-CRQDP---DSRATLPARKETTASLG 249
DB      311  QAAAEAGSSRDVAVNRSHGOLKTDEQGLNTHGASEISEQDMLGDSQFSKRTSDTTTETA 370

QY      250  SDRSRKSSLLPSIRAYKSNVIVASQVGL-----SHSDSLAQORHEIELFRARKLAKS 304
DB      371  PGKGKFLS-----GSNTGLDYIKFTWKRLRSHS---ROYVSLGHMNRERKAAQ 416

QY      305  LAILLAFAAICWAPYSLTTVYSPFPERNLTKSTWYHTAFWLQWNSFVNVPFLVPLCHKR 364
DB      417  LGFIMAFILCWIPIFYFFWVIAFC--KNCCNEHLHMFTIWLGYINSTLPLIYPLCNEH 474

QY      365  FOKAFKLILPVR 376
DB      475  FKKTFKRILHIR 486

RESULT 9
US-11-127-877-51
; Sequence 51, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590

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; Publication No. US20050266522A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Amine Receptor
; FILE REFERENCE: PF188D1C2
; CURRENT APPLICATION NUMBER: US/10/875,716
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 09/988,745
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 09/314,006
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 08/467,559
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-716-10

Query Match      17.5%; Score 356.5; DB 6; Length 353;
Best Local Similarity 27.2%; Pred. No. 1.4e-24;
Matches 101; Conservative 66; Mismatches 139; Indels 65; Gaps 11;

QY 20 LMSLLAIAIMLGNVVILAFIVDRNLHRSNYFFLNLAIAADPFVGAIAIP--LYIPSSLT 77
DB 31 LUTLLAVIVFGNVLCMAVSREKALQTTNYLIIVSLAVADLLVATLVMPWVYL--EVVG 89

QY 78 YMTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVYRAQHSQGTWKIATQVMA 137
DB 90 EKKFSRIHCDIFVTLDMVMCTASILNLCASIDRYTAVAMPMLNTRYSSKRRVTVMISI 149

QY 138 VNIFFSMTNGPML--ISDSWQNSSTTECPGPKKQWTFALPTSLLLEPLIPLIVAYFSAHI 196
DB 150 VVWLSPTISCPLLFGLNADQNECIIANPAFV-----VYSSIVSFVFPFIVTLVYIKI 203

QY 197 YNSLWKREKLSRCLSHPLVPSDSSSDHGHSCRDQDPSRATL--PARKETTASLGS DKSR 254
DB 204 YIVLRERRK-----RVNTKSSRAFRH-----LRAPLKEARRKN---GHAKDH 246

QY 255 RKSSLLPSIRAYKNNSVIAKMGFLSHSDSLAQOREHIELFRARKLAISLAIIAALPAI 314
DB 247 PKIAKFEIQTWPNGKT-----RTSLKTSRRKLSQKQKKAQWMAIVLGVFII 296

QY 315 CWAPVSLT-----TVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFLYPLCH 362
DB 297 CWLPFPFTHILNHCDCNIPPVLYSAFT-----WLGTVNSAVNPIIYTFN 342

QY 363 KRPQKAPLKI 373
DB 343 IEFKRAFLKI 353

RESULT 14
US-11-165-024-3
; Sequence 3, Application US/11165024
; Publication No. US20050266527A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Receptor HIBEP51
; FILE REFERENCE: PF187D1C2
; CURRENT APPLICATION NUMBER: US/11/165,024
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 10/006,394
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 09/228,420
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 08/465,971
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 350

; Publication No. US20050266522A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Amine Receptor
; FILE REFERENCE: PF188D1C2
; CURRENT APPLICATION NUMBER: US/10/875,716
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 09/988,745
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 09/314,006
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 08/467,559
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-716-10

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Best Local Similarity 26.7%; Pred. No. 3.9e-23;
Matches 102; Conservative 62; Mismatches 129; Indels 89; Gaps 14;

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DB 29 SLQVTLTLVCLAGLLMLLTVFGNVLVIIAVFTSRALKAPQNLFLVSLASADILVATLVIP 88

QY 70 LYIPSS--LTYMTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVYRAQHSQGT 128
DB 89 FSLANEWMGYWYFGKAWCEIYIALDVLPCTSSIVHLCAISLDRYWSTQVAENLKRTPR 148

QY 129 WKIATQVMAVWIFSPMTNGPMLISDSW-----QNSTTECEPGFLKKYFALPTSLLLEP 182
DB 149 -RIKAIITVWISAVISFPPLISIEKGGGGQGPAPBPRCEIND-QKWY-VISSCIGSF 205

QY 183 LPILLIVAYFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCRDQDPSRATLPARK 242
DB 206 PAPCLIMILVYVRIYQIAKRTR-----VPPS-----RRGPDVAVAPPG-- 244

QY 243 ETTASIGSDKSRKSSLLPSIRAYKNNSVIAKMGFLSHSDSLAQOREHIELFRARKLA 302
DB 245 -----GLOGRGRSASGLPRRAGAG-----QNR-----KRFT 273

QY 303 KSLAIIAALFAICWAP-----YSLTTV-----IYSPFPERNLTKSTWYHTAFWLQWNS 351
DB 274 FVLAVVIGVFWVWCPFPFPFPTTLTAVGCVPRTPLPKF-----FMFGVCNS 319

QY 352 FVNPFLYPLCHKRFQKAPLKI 373
DB 320 SLNPVIYITFNDFRAFKIL 341

RESULT 15
US-11-232-805-46
; Sequence 46, Application US/11232805
; Publication No. US20060073508A1
; GENERAL INFORMATION:
; APPLICANT: Small, Kersten M.
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-42D
; CURRENT APPLICATION NUMBER: US/11/232,805
; CURRENT FILING DATE: 2005-09-22
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 46
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-232-805-46

Query Match      16.6%; Score 338; DB 7; Length 458;
Best Local Similarity 25.9%; Pred. No. 9e-23;
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DB 54 LAAVGVGLIVFTVGVGNLVIIAVLTSRALRQNLFLVSLASADILVATLVMPFSLANEL 113

QY 77 -TYMTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVYRAQHSQGTWKIATOM 135
DB 114 MAYWFGQWCVGYIALDVLPCTSSIVHLCAISLDRYWSTQVAENLKRTPR-RVKATI 172

QY 136 VAVWIFSPMTNGPMLISDSWQNSSTTECEPGFLKKYFALPTSLLLEPLIPLIVAYFSAH 195
DB 173 VAVWLSISAVISFPPLVSLVYRQPDGAAYPCGLNDETWYILSSCIGSFAPCLIMGLVYAR 232

QY 196 IYWSLWKREKLSRCLSH-----FVLPSDSS-----SSDHGHSCRDQDPSRATLPA 240
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%

Maximum Match 100%
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NCPU=6 -ICPU=3 -NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	694.5	34.1	1239	3	US-09-891-053-2
5	694.5	34.1	2700	3	US-09-891-053-5
6	689.5	33.9	1335	2	US-08-985-090-3
7	689.5	33.9	1335	3	US-09-165-543-3
8	689.5	33.9	1335	3	US-09-167-354-6
9	689.5	33.9	1335	3	US-09-642-855-6

10	689.5	33.9	1335	3	US-09-642-514-6	Sequence 6, Appli
11	689.5	33.9	1335	3	US-09-642-852-6	Sequence 6, Appli
12	689.5	33.9	2050	3	US-03-891-053-21	Sequence 21, Appl
13	689.5	33.9	2665	3	US-03-943-016-5059	Sequence 5059, Ap
14	689.5	33.9	2689	2	US-08-985-090-1	Sequence 1, Appli
15	689.5	33.9	2689	3	US-09-165-543-1	Sequence 1, Appli
16	689.5	33.9	2699	3	US-09-167-354-5	Sequence 5, Appli
17	689.5	33.9	2699	3	US-09-642-855-5	Sequence 5, Appli
18	689.5	33.9	2699	3	US-09-642-514-5	Sequence 5, Appli
19	689.5	33.9	2699	3	US-03-642-852-5	Sequence 5, Appli
20	681.5	33.5	1338	3	US-09-165-543-6	Sequence 6, Appli
21	681.5	33.5	1953	3	US-09-891-053-26	Sequence 26, Appli
22	681.5	33.5	3244	3	US-09-165-543-4	Sequence 4, Appli
23	609.5	29.9	1056	3	US-09-524-162-1	Sequence 1, Appli
24	546	26.8	1086	2	US-08-985-090-6	Sequence 6, Appli
25	546	26.8	1086	3	US-03-165-543-33	Sequence 33, Appli
26	546	26.8	2218	2	US-08-985-090-4	Sequence 4, Appli
27	546	26.8	2218	3	US-09-165-543-31	Sequence 31, Appli
28	403.5	19.8	1913	3	US-09-016-434-1314	Sequence 1314, Ap
29	398.5	19.6	1773	3	US-09-826-509-516	Sequence 516, App
30	397	19.5	2261	3	US-03-016-434-1176	Sequence 1176, Ap
31	392	19.3	1599	3	US-03-826-509-520	Sequence 520, App
32	389.5	19.1	1386	3	US-09-016-434-1339	Sequence 1339, Ap
33	388.5	19.1	1956	2	US-08-313-553-6	Sequence 6, Appli
34	388.5	19.1	1956	3	US-08-767-993-6	Sequence 1411, Ap
35	386.5	19.0	1742	3	US-03-016-434-1411	Sequence 11, Appl
36	385.5	18.9	2004	2	US-08-722-001-11	Sequence 1368, Ap
37	385.5	18.9	2290	3	US-09-016-434-1368	Sequence 512, App
38	385.5	18.9	2536	3	US-09-919-039-5	Sequence 158, App
39	384.5	18.9	1422	3	US-09-826-509-512	Sequence 5, Appli
40	384.5	18.9	4008	3	US-09-976-594-158	Sequence 5, Appli
41	384	18.9	1639	2	US-08-334-598-5	Sequence 5, Appli
42	384	18.9	1639	2	US-08-228-932-5	Sequence 5, Appli
43	384	18.9	1639	2	US-08-468-939-5	Sequence 5, Appli
44	384	18.9	1639	2	US-08-406-855A-5	Sequence 5, Appli
45	384	18.9	1639	2	US-08-722-190-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monama, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Alignment Scores:
Pred. No.: 3.68e-129 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3

US-10-626-398-10 (1-389) x US-09-414-010-1 (1-1173)


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Db 433 TAGTGAATGGCCATATCTTAGTTTCAGATCTTGGAGGATGAAGTAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysLeuTyrPheLeuLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGATTTTTCGGAATGGTACATCTTGGCATCATCATCTTGGATTCGTG 552
Qy 184 IleProIleLeuLeuValalaTyPheSerAlaHisIleTyrTrpSerLeuTyrLysArg 203
Db 553 ATCCAGATCATCTTAGTCGCTATTTCACATGAATATTTATGGAGCCTGTGAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCAAGCATCTCTGAGCTGACTGCT--GTCTCTTCAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCATCGACAGA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCTGCTCTCTTTCATTCAGAGACAGAGGAGAGAGTAGTCTCATGTTTCTCTCA 789
Qy 264 ArgAlaTyLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACATTCCTTCCAAATGGGTCTCTTCCCATCAGAT 849
Qy 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTTTCACCAAGGAGCATCTTGAACCTGCTTAGCCAGGAGATTAGCCAA 909
Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACCTGGCCATCTCTTAGGGGTTTTGCTGTGCTGGCTGCCATATCTCTGTTCACA 969
Qy 324 ValIleTySerPhePheProGluArgAsnLeuThrLysSerThrTrpTyHisThrAla 343
Db 970 ATTGCTCTTTCATTTTATCTCTCAGCACAGCTCTCAATCAGTTGGTATAGATGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyProLeuLysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTCAATCTCTTGTCAATCTCTTTGTATCCATCTGTGCACAA 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAGCAACCTCTTACCACAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTCT 1170

RESULT 3
US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13
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Alignment Scores:
Pred. No.: 3,68e-129 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3
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US-10-626-398-10 (1-389) x US-09-875-076-13 (1-1173)

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Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAAATCAATTTATCATCACTAAGCACCTCGTGTACTTTAGCATTTTATGTCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGTATATAATGCTAGGAAATGCTTTGGTCACTTTTAGCTTTTGTGTGACAAA 132
Qy 44 AsnLeuArgHisArgSerAsnTyPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCTGATCTTCTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyIleProSerSerLeuThrTyTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATCTCTTTGTACATCCCTCACAGCTGTTTGAATGGATTTTGAAGA 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyTrp 103
Db 253 GAAATCTGTGTATTTTGGCTCACTGACTATCTGTATGTACAGCATCTGTATATATAC 312
Qy 104 IleValLeuIleSerTyAspArgTyGlnSerValSerAsnAlaValTyTrpArgAla 123
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Db 313 ATTGTCCTCATCAGCTATGATCGATACCTGTGCTCAAAATGCTGTCTTTATAGAAT 372
Qy 124 GlnHisSerGlyThrTyrLysAlaThrGlnMetValAlaValTyrPheSerPhe 143
Db 373 CAACATATCGGGCTCTGAAGATTCTTACTCTGATGGTGGCGTTTGGTGTCTGGCCCTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGAATGGCCCAATGATTCAGTTCAGAGTCTTGGAGGATGAGTAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTACATCTTCCATCAGATCATCATCTTCTGGAATTCGTG 552
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTyrSerLeuTyrLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTAATTCACATGAAATATTTATGTGAGCCTGTGGAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGTGGCCAAAGCCATCTCGACTGACTGCT---GTCTCTTCCCAATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCAATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCCTGATCCTTTTCATTCAGAGACAGAGGAGAAAGATGTCTCATGTTTTCCTCA 789
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATGCAATACATATGCTTCCAAATGGTCTCTTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluIlePheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCCAAAGGGAACATGTTGAACTGCTTAGAGCCAGGAGATTAGCCAAAG 909
Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTyrAlaProTyrSerLeuThr 323
Db 910 TCATGGCCATCTCTTAGGGGTTTGTGCTTTGTGGGTCCATATCTCTGTTTCCACA 969
Qy 324 ValIleTyrSerPheProGluArgAsnLeuThrLysSerThrTyrTyrHisThrAla 343
Db 970 ATTGCTCTTCATTTTATCTCTCAGCAACAGGTCTTAATCAGTTTGGTAGAATTGCA 1029
Qy 344 PheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTTCATTCCTTTGTCAATCCTCTTTTGTATCCATTGTGTACAAAG 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAGGCTTTCTGAAATATTTTGTATAAAGAAACCACTCTACCATCAAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170
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RESULT 4

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; US-09-891-053-2
; Sequence 2, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yuseki
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
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; CURRENT APPLICATION NUMBER: US/09/891.053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-891-053-2

Alignment Scores:
Pred. No.: 8.19e-64 Length: 1239
Score: 694.50 Matches: 159
Percent Similarity: 55.4% Conservative: 66
Best Local Similarity: 39.2% Mismatches: 130
Query Match: 34.1% Indels: 51
DB: 3 Gaps: 12

US-10-626-398-10 (1-389) x US-09-891-053-2 (1-1239)
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGCTTCGCGTGGCTGGACCGCTGC-----CTGGCTGGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCTGTGGCCACAGTACTGGGACGCGCTGCTCATGCTCGCTTCGTGGCGAT 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 187 TCGAGCTCTCGCAGCCAGAACAACTTTCTGTCTCAACCTCGCATCTCCGATCTCTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrThrSer 81
Db 247 GTGGTGCTTCTGCATCCCATTTGATGATGATGCTGTGCTGACCGCGCTGGACCTC 306
Qy 82 GlyLysGlnAlaCysValPheTyrPheLeuThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 307 GGCCTGGGCGCTCTGCAAGCTGTGGTGGTGTAGACTACCTACTGTGTGCTCTCGGTC 366
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyr 121
Db 367 TTCAACATCTGATCTCATGATGACCGATTTCTGTGATGATGATGATGATGATGATG 426
Qy 122 ArgAlaGlnHisSerGlyThrTyrLysIleAlaThrGlnMetValAlaValTyrIlePhe 141
Db 427 AGGCGCCAGCAGGGGGACACGAGAGCGCGCTTCGGAAGATGCGACTGGTGGGTGTG 486
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTyrGln----- 157
Db 487 GCCTTCTGCTGTATGGGCGCTGCCATCTCTG-----AGTTGGAGTAGTACCTGTCT 537
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysIleTyrTyrPheAla 174
Db 538 GGCAGTTTCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGCTGATCTTC 597
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 598 ATCAGGCGCTCCACCCCTCGAGTTCTTCAAGCCCTTCTCTCAGCGTGTACCTCTTCA 657
Qy 195 HisIleTyrThrSerLeuTyrLysArgGluLysLeu-----SerArgCysLeuSer 211
Db 658 AGCATCTTACCTGAACATCCAGAGCGCACCCGCTTTCGGCTTGTATGGGGCGGTGAGG 717
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Qy 212 HisProValLeuProSerAspSerSerSerSer----- 222
Db 718 GGGCCAGAAACCCACCAAGGCGCCAGCCCTCGCCACCTCCAGCTCCCGCCAGCTGCTGG 777
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThr 237
Db 778 GGCTGCTGGCCAAAGGCGCATGGCGAGCC----- 807
Qy 238 LeuProAlaArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgLysSer 257
Db 808 ATGCCGTTGCACAGCTCTGGCAGCTCTCAAGGGGCGCACTGAGAGGCCACGC----- 858
Qy 258 SerLeuLeuProSerIleArgAlaTyrllysAsnSerAsnValIleAlaSerLysMetGly 277
Db 859 TCACCTCAAAAGGGGCTCCAAAGCCATCAGCATCTTCAGCATCCCTGGAGAGCGCATGAAG 918
Qy 278 PheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHisIleGluLeuPheArg 297
Db 919 ATGGTGTCACAGGC-----ATCACCCAGCGC-----TTCGGGCTGTCGGG 960
Qy 298 AlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAla 317
Db 961 GACAAAGAGTGGCGCAAGTCGCGCCATCATCGTGAGCATCTTTGGGCTCTGCTGGCG 1020
Qy 318 ProTyrlSerLeuThrValIleTyrlSerPhePheProGluArgAsnLeuThrLysSer 337
Db 1021 CCGTACAGCTCTTAATGATCCGAGCTCTTCGCCATGGCCGCTGCATC---CCCGAT 1077
Qy 338 ThrTrpTyrlHisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeu 357
Db 1078 TACTGGTACGAGAGCTCTTCTGGCTCTGTGGGCAACTCGGGCGTCAACCCGCTCTC 1137
Qy 358 TyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArg 377
Db 1138 TACCACCTGTCGCACTACAGCTTCGCGAGAGCTTCACCAAGCTCTCTGCGCCCGCAGAG 1197
Qy 378 GlnSerThrProProHis 383
Db 1198 CTCAGGTTCAGCCCCAC 1215

RESULT 5
US-09-891-053-5
; Sequence 5, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIORITY APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (351)...(1589)
; NAME/KEY: misc_feature

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; LOCATION: (1)...(2700)
; OTHER INFORMATION: n = A, T, C or G
US-09-891-053-5

Alignment Scores:
Pred. No.: 2,936-63 Length: 2700
Score: 694.50 Matches: 159
Percent Similarity: 55.4% Conservative: 66
Best Local Similarity: 39.2% Mismatches: 130
Query Match: 34.1% Indels: 51
DB: 3 Gaps: 12

US-10-626-398-10 (1-389) x US-09-891-053-5 (1-2700)
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 426 GCGCGCGGCTTCTCGGCTGCTGACCGCTGC-----CTGGCTGGCGCTCATGGCG 476
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAlaPheIleValAsp 42
Db 477 CTGCTCATCGTGGCCACAGTACTGGGCAACGCGCTGCTCAGCTCGGCTTCGTGGCGAT 536
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrlPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 537 TCGAGCTTCGCGACCCAGAACACTCTTCTGCTCAACCTCGCCATCTCCGACTTCCTC 596
Qy 63 ValGlyAlaIleAlaIleProLeuTyrlProSerSerLeuThr-----TyrlTrpThrSer 81
Db 597 GTGGGTGCTTCTGCATCCCATTCAGTACCTATGCTGCTGACCGCGCGTGGACCTTC 656
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrlLeuLeuCysThrAlaSerVal 101
Db 657 GCGCGGGGCTCTGCAAGCTGTGGCTGGTGTAGTACCTACTGTGCTCTCTCGGTC 716
Qy 102 TyrAsnIleValLeuIleSerTyrlAspArgTyrlGlnSerValSerAsnAlaValTrpTyrl 121
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Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 777 AGGCCCCAGAGGGGGACAGAGCGGCGCTTCGGAAGATGGCACTGGTGTGGGTGTG 836
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 837 GCCTTCTGCTGTATGGCGCTGCCATCTGT-----AGTTGGAGTACCTGTGTGGT 887
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTyrlTrpPheAla 174
Db 888 GGCAGTTCATCCCGAGGGCCACTGTATGCTGAGTTCTTCTACAACTGGTACTTCTC 947
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrlPheSerAla 194
Db 948 ATCAGCGCTCCACCTCGAGTCTTTCACGCGCTTCCTCAGCGTTACCTCTTCAACCTC 1007
Qy 195 HisIleTyrlTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeuSer 211
Db 1008 AGCATCTACCTGAACATCCAGAGCGCACCGCGCTTCGCTGTGATGGGGCGCGTAGGCT 1067
Qy 212 HisProValLeuProSerAspSerSerSer----- 222
Db 1068 GGGCCAGAACCCCAACAGATGCCAGCCCTCGCCACTCCAGCTCCCGCCAGCTGTGG 1127
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThr 237
Db 1128 GGCTGCTGGCCAAAGGCGCATGGCGAGCC----- 1157
Qy 238 LeuProAlaArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgLysSer 257
Db 1158 ATGCCGTTGCACAGCTCTGGCAGCTCTCAAGGGGCGCACTGAGAGGCCACGC----- 1208
Qy 258 SerLeuLeuProSerIleArgAlaTyrllysAsnSerAsnValIleAlaSerLysMetGly 277
Db 1209 TCACCTCAAAAGGGGCTCCAAAGCCATCAGCATCTTTCAGCATCCCTGGAGAGCGCATGAAG 1268

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1000	GAGAAAGCGCATGAAGATGGTGTCCAGAGCTTCACC-----CAGCGC	1041	
Qy	293	IleGluLeuPheAraGalaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPhe	312
Db	1042	TTTCGGGTGTCTTCGGGACAGAAAGTGCCAAAGTCGTGGCGGTCACTGGAGCATCTTT	1101
Qy	313	AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg	332
Db	1102	GGGCTCTGCTGGGGCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGC---CATGGC	1158
Qy	333	AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe	352
Db	1159	CACTCGCTCCCTGACTACTGTGTAGCAAACTCTCTCTGGCTCTCTGTGGGCCCACTCGGCT	1218
Qy	353	ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle	372
Db	1219	GTCAAACCTGTCTCTACCTCTCTGTGCACACACAGCTTCGCCGGGGCTTCACCAAGCTG	1278
Qy	373	LeuProValArgArgGlnSerThrProHisAsn	384
Db	1279	CTCTGCCCCCAAGAGCTCAAAATCCAGGCCCCACACAGC	1314

RESULT 7

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00001 /
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentm Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543

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Alignment Scores:		
Pred. No.:	3.15e-63	Length: 1335
Score:	689.50	Matches: 161
Percent Similarity:	53.5%	Conservative: 70
Best Local Similarity:	37.3%	Mismatches: 132

Query Match:	33.9%	Indels:	69
DB:	3	Gaps:	13
US-10-626-398-10 (1-389) x US-09-165-543-3 (1-1335)			
Qy	3	AlaasnAnSerThrIleAlaLeuThrSerIleIleIleSerLeuThrPheLeuMetSer	22
Db	76	GC GCGCGGCTTC TCGG CAGCCTG GACCGCGGTG-----CTGGCGCGCTCATGGCG	126
Qy	23	LeuLeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAlaPheIleValAsp	42
Db	127	CTGCTCATCTGGCCACCGTGCTGGGCAACGCGTGCTCATGCTCGCTTCGTGGCGCCGAC	186
Qy	43	ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe	62
Db	187	TCGAGCCTCGCGACCCAGAACAACTTCTCTGCTCAACCTCGGCATCTCGGACTTCCTC	246
Qy	63	ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer	81
Db	247	GTGCGCGCCTTCGTCATCCCACTGATGTATGTAACCTACGTGCTGCAGCGCCGTGGACCTTC	306
Qy	82	GlyIysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuLeuCysThrAlaSerVal	101
Db	307	GGCGGGGCGCTCTGCAAGCTGTGGTGTAGTGGACTACCTGCTGTGCACCTCTCTCTGCC	366
Qy	102	TyrAsnIleValIleIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr	121
Db	367	TTCAACATCTGCTCATCAGTACGACCGGCTTCTGTGCGGTCAACCGAGCGGTCTCATAC	426
Qy	122	ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe	141
Db	427	CGGCGCCACGAGGGTGACGCGCGGGGAGTGGGGAAGATGCTGTGTTGGGTGCTGCTG	486
Qy	142	SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln-----	157
Db	487	GCCTTCTGCTGTACGACGACGAGCATCTG-----AGCTGGGAGTACCTGTCCCGG	537
Qy	158	---AsnSerThrThrGlu-----CysGluProGlyPheLeuIleIleTyrTrpPheAla	174
Db	538	GGCAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTCAACACTGGTACTTCCTC	597
Qy	175	LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla	194
Db	598	ATCAGCGCTCCACCTGGAGTCTTTACGCCCTCTCTCAGCGTCACTTCTTTAACTCCTC	657
Qy	195	HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu	210
Db	658	AGCATCTACCTGAACATCCAGAGCGCACCCGCTTCGGGTGGATGGGCTCGAGAGGCA	717
Qy	211	SerHisProValIleProSerAspSerSerSer-----	222
Db	718	GCGGCGCCCGAGCCCTCTCCGAGGGCCAGCCCTCACCCACCGCTGGCTGTCTGG	777
Qy	223	-----AphHisGlyHisSerCysArgGlnAspProAspSerArg-----	235
Db	778	GGCTGTGCGCAGAAGGGGCACGGGGAGGCCATG-----CCGCTGCACAGGTATGGG	828
Qy	236	-----AlaThrLeu-----	238
Db	829	GTGGGTGAGCGCGCGGTAGCGCTGCAGCGCGGGAGGCGACCTTCGGGGGTGGCGTGGG	888
Qy	239	-----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys	252
Db	889	GGCGGCTCCGTGGCTTCAACCCTCAGCTCCGGCAGCTCTCTCGAGGGGCATCGAGGG	948
Qy	253	SerArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIle	272
Db	949	CCGGGC-----TCACTCAAGAGGGGCTCCAAGCGCTCGCGCTCTCTCGGCTCACTG	999
Qy	273	AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis	292
Db	1000	GAGAAGCGCATGAAGATGGTGTCCCAAGCTTTCACC-----CACGCG	1041

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Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPhe 312
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Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrValIleTyrSerPhePheProGluArg 332
Db 1102 GGGCTGCTGGGCCCCCACCACAGCTGCTGATGATCATCGGGCGGCTGC---CATGGC 1158
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1159 CACTGCGCTCGCTACTACTGTGTACAAACCTCTCTGGCTCTGTGGGCCAACTCGGCT 1218
Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1219 GTCAACCTGCTCTACCTCTGTGTGTCACACAGCTTCCGGCGGCTTTCACCAAGCTG 1278
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1279 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGC 1314

RESULT 8
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 613659
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-6

Alignment Scores:
Pred. No.: 3.15e-63 Length: 1335
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13

US-10-626-398-10 (1-389) x US-09-167-354-6 (1-1335)
Qy 3 AlaAsnSerThrIleAlaLeuThrSerIleLysSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGCTTCTCGGACAGCTGGACCGCGTG-----CTGGCGGCGCTCATGGC 126
Qy 23 LeuLeuAlaIleAlaMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCGTGGCCACGGTCTGGGCAACGCGTGTCTGCTCGCTTCGTGGCCGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhe 62
Db 187 TCGAGCTCCGACCCAGAACAACTTCTCTGCTCAACCTCGGCATCTCCGACTTCTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 247 GTCCGGCGCTTCTGCATCCCACTGTATGATACCTACCTGTCGACAGCGCGCTGACCTC 306
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 307 GCGCGGCGCTCTGCAGACTGTGGCTGGTAGTGAGCTACCTGTGCTGTGACCTCTCTGCC 366
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RESULT 9

US-09-642-855-6

; Sequence 6, Application US/09642855

; Patent No. 6413743

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; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6

Alignment Scores:
Pred. No.:          3,15e-63           Length:       1335
Score:              689.50            Matches:      161
Percent Similarity: 53.5%             Conservative: 70
Best Local Similarity: 37.3%         Mismatches:   132
Query Match:        33.9%            Indels:       69
DB:                  3                Gaps:        13

US-10-626-398-10 (1-389) x US-09-642-855-6 (1-1335)

QY    3 AlaAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
      ::: :::: ||| |||||:||||: ||| |
Db    76 GCGCGGGCTTCGCGACCTGGACCGGGTG-----CTGGCGGGCTCATGGCG 126

QY    23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
      :|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    127 CTGCTCATGTGCCACGCGTGTGGCCAACGGCTGGTGCATGTCTCGCTTCGTGGCGCAG 186

QY    43 ArgAsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
      ::|||:|||: ||::::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    187 TCGAGCGCTCGCACCCAGAACAACTTCTTCTGTCAACTCGCCATCTCCGACTTCCTC 246

QY    63 ValGlyAlaIleAlaIleProLeuTyrrileProSerSerLeuThr---TyrTrpThrSer 81
      :|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    247 GTGCGGGCGCTTCGTGATCCCACTGATATGAACCTACGTGTGCACAGCGCGCTGCACCTTC 306

QY    82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrrLeuLeuCysThrAlaSerVal 101
      ::|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    307 GGCGGGGGCTCTGCAAGCTGTGGCTGTGTAGTGAGTACTCTGTGTGCACCTCTCTGTGCG 366

QY    102 TyrAsnIleValLeuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTyrrTyrr 121
      ::|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    367 TTCAAATCATGTCTCATCAGCTACAGACGCTTCTCTGTGGGTACCAGGCGGTCTCATAC 426

QY    122 ArgAlaGlnHisSerGlyTyrrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
      :|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    427 CGGGCCCACAGAGGTGCACAGCGGGCGGCGAGATGCTGTGGTGGGGTGGTGGT 486

QY    142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
      ::|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    487 GCCTTCTCTGTACAGGACCAACCATCTGTG-----AGCTGGAGTAGCTGTGCGGG 537

QY    158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysIlysTyrrTyrrPheAla 174
      ::|||::|||: |||::|||: |||::|||: |||::|||: |||::|||: |||::|||:
Db    538 GGCAGCTCCATCCCCAGGGCCACATGCTATGCCGAGTTCTTCTACAACTGGTACTTCTCCT 597

QY    175 LeuProThrSerLeuLeuCluPheLeuIleProIleLeuValAlaIleTyrrPheSerAla 194
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Db    598 ATCAGCGGCTTCCACCCCTGGAGTCTTTTACGGCCCTTCTCTCAGCGTCACTCTTTTAACCTC 657

QY    195 HisIleTyrrTrpSerLeuTriPylsArgGluLysLeu-----SerArgCysLeu 210
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Db      658  AGCATCTACCTGAACATCCAGAGCGGCACCGGCTCCGGCTGGATGGGCTCGAGAGGCA 717
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Qy      211  SerHisProValLeuProSerAspSerSerSerSerSerSerSerSerSerSerSerSer 222
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Db      718  GC CGGCCCGAGCCCGCTCCCGAGGCGCCAGCCCTCACACCCCGCTGGCTGCTGG 777
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      223  -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      778  GGCTGCTGGCAGAGGGGCACGGGGAGGCCATG-----CGCTGCACAGGTATGGG 828
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Qy      236  -----AlaThrLeu----- 238
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      829  GTGGGTGAGCGCGCGTAGCGCTGAGCGCGGGAGCGGACCTCGGGGGTGGCGTGGG 888
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      239  -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      889  GGCGGCTCCGTGGCTTCACCCACCTCCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGG 948
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      253  SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAanSerAanValIle 272
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      949  CCGCGC-----TCACACAAGAGGGGCTCCAAGCGCTCGCGGCTCCTCGGCCTCGCTG 999
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      273  AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnGlnArgGluHis 292
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Db      1000  GAGNAGCGCATGATGGTGTCCAGAGCTTCACC-----CAGCGC 1041
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Qy      293  IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaLeuLeuAlaAlaPhe 312
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1042  TTTCCGGCTGCTCGGGACAGAAAGTGCGTGGCGCTCATCGTGAGCATCTTT 1101
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      313  AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
      ::||| ::||| |||| |||| |||| |||| |||| |||| ||||
Db      1102  GGGCTGTGCTGGGCCCATACACGCTGCTGATCATATCGGGCGCGCTGC---CATGGC 1158
      ::||| ::||| |||| |||| |||| |||| |||| |||| ||||
Qy      333  AsnLeuThrLysSerThrTyrTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
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Db      1159  CACTGGCTCCCTGACTACTGGTACGAAACCTCCTTCCTGGCTCCTGTGGCCAACTCGGCT 1218
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Qy      353  ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
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Db      1219  GTCAACCCCTGCTCCTACCCCTCTGTGCCACACAGCTTCGCGCGGGCTTCACCAAGCTG 1278
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      373  LeuProValArgArgGlnSerThrProProHisAan 384
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1279  CTCTGCCCCCAGAAGCTCAAAATCCAGCCCCCAGAC 1314
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RESULT 10
US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

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Db      658  AGCATCTACCTGAACATCCAGAGCGGCACCGGCTCCGGCTGGATGGGCTCGAGAGGCA 717
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Qy      211  SerHisProValLeuProSerAspSerSerSerSerSerSerSerSerSerSerSerSer 222
      :: |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      718  GC CGGCCCGAGCCCGCTCCCGAGGCGCCAGCCCTCACACCCCGCTGGCTGCTGG 777
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      223  -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
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Db      778  GGCTGCTGGCAGAGGGGCACGGGGAGGCCATG-----CGCTGCACAGGTATGGG 828
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Qy      236  -----AlaThrLeu----- 238
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      829  GTGGGTGAGCGCGCGTAGCGCTGAGCGCGGGAGCGGACCTCGGGGGTGGCGTGGG 888
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      239  -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
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Db      889  GGCGGCTCCGTGGCTTCACCCACCTCCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGG 948
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Qy      253  SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAanSerAanValIle 272
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      949  CCGCGC-----TCACACAAGAGGGGCTCCAAGCGCTCGCGGCTCCTCGGCCTCGCTG 999
      |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy      273  AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnGlnArgGluHis 292
      ::||| ::||| |||| |||| |||| |||| |||| |||| ||||
Db      1000  GAGNAGCGCATGATGGTGTCCAGAGCTTCACC-----CAGCGC 1041
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Qy      293  IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaLeuLeuAlaAlaPhe 312
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Db      1042  TTTCCGGCTGCTCGGGACAGAAAGTGCGTGGCGCTCATCGTGAGCATCTTT 1101
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Qy      313  AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
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Db      1102  GGGCTGTGCTGGGCCCATACACGCTGCTGATCATATCGGGCGCGCTGC---CATGGC 1158
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Qy      333  AsnLeuThrLysSerThrTyrTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
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Db      1159  CACTGGCTCCCTGACTACTGGTACGAAACCTCCTCTCGGCTCCTGTGGGCCAATCGGCT 1218
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Qy      353  ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
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Db      1219  GTCAACCCCTGCTCTACCCCTCTGTGCCACACAGCTTCGCGCGGGCTTCACCAAGCTG 1278
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Qy      373  LeuProValArgArgGlnSerThrProProHisAan 384
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Db      1279  CTCTGCCCCCAGAAGCTCAAAATTCAGCCCCCAGC 1314
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RESULT 10
US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

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Alignment Scores:

Pred. No.: 3,15e-63 Length: 1335
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13

US-10-626-398-10 (1-389) x US-09-642-514-6 (1-1335)

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Qy 3 AlaAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGCTTCTCGGAGCCTGGACCGCGTG-----CTGGCGCGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCTGGCCACCGGTGCTGGCAACGCGTGTGCTCATGCTCGCTTCTGGCGCGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 187 TCGAGCTTCGCGCCCGCAGACACTTCTCTGCTCAACCTCGCATCTCGACTTCTCTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr-----TyrTrpThrSer 81
Db 247 GTCGCGCTTCTGCATCTCCACTGTATGTACCTTACCTTACCTGTGCTGACAGCGCGTGCACCTTC 306
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrIleLeuLeuCysThrAlaSerVal 101
Db 307 GCGCGCGCGCTCTGCAAGCTGTGGCTGTGTAGTGACCTACCTGTGTGCACCTCTCTCTGCC 366
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 367 TTCAACATGTGTCTATCAGCTACGACGCTCTCTGCTCGGTGCTGCGCGCGGTCTCATAC 426
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 427 CGGCGCCAGCAGGTGTACAGCGCGCGCAGTGGGGAAGATGCTGTGTGTGTGGTGTGCTG 486
Qy 142 SerPheMetThrAnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 487 GCCTTCTCTGTGTACGACGACGACCTCTG-----AGCTGGGAGTACCTGTCTCGCGG 537
Qy 158 --AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpTyrPheAla 174
Db 538 GGCAGCTCCATCCCGAGGCGCATCTGTATGCCAGTTCCTTACAACTGGTACTTCTCTC 597
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 598 ATCAGCGCTTCCACCTGGAGTCTTTAGCGCTTCTCTCAGCGTCACTTCTTTTAACTCTC 657
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 658 AGCATCTACTCTGAACATCCAGAGCGCACCGCTCCGCTCGGCTGGATGGGCTCGAGAGGCA 717
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 718 GCGCGCCCGAGCCCTCTCCGAGCGCCAGCCCTCACACCCCGCCCTGGCTGTGG 777
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 778 GGCTGCTGGCAGAGGGGCACGGGAGGCCATG-----CGCTGCACAGGTATGGG 828
Qy 236 -----AlaThrLeu----- 238
Db 829 GTGGGTGAGCGCGCTAGGCGCTGAGCGCGGGAGCGACCTCTCGGGGTGGCGGTGGG 888
Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 889 GCGCGCTCCGTGGCTTCAACCTTCCAGCTCCGCGAGCTCTCTGAGGGGACATGAGAGG 948
Qy 253 SerArgArgLysSerSerLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 949 CCGCGC-----TCACTCAAGAGGGGCTCCAAGCGTCCGCGCTCTCGCGCTCGCTG 999
```

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Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1000 GAGAGCGCATGAGATGGTGTCCAGAGCTTCACC-----CAGCGC 1041
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaPhe 312
Db 1042 TTTCCGGCTGTCTCGGACACAGGAAGTGGCAGCTCGTCCGCTCATCGTGCATCTTT 1101
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1102 GGCTCTGTGTGGCCCATACACGCTGTGATCATCTCGGCGCGCTGC-----CATGGC 1158
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1159 CATGGTCCCTGACTACTGTTACGAAACCTCTCTTCTGGCTCTGTGGGCAACTCGGCT 1218
Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1219 GTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCGCGCGGCTTCCACCAAGCTG 1278
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1279 CTCTGCCCGCAGGAAGCTCAAAATCCAGCCCGCACAGC 1314
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RESULT 11

US-09-642-852-6
; Sequence 6, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE OF INVENTION: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-852-6

Alignment Scores:
Pred. No.: 3,15e-63 Length: 1335
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13

US-10-626-398-10 (1-389) x US-09-642-852-6 (1-1335)

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Qy 3 AlaAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGCTTCTCGGAGCCTGGACCGCGTG-----CTGGCGCGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCTGGCCACCGGTGCTGGCAACGCGTGTGCTCATGCTCGCTTCTGGCGCGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 187 TCGAGCTTCGCGCCCGCAGACAACTTCTCTGCTCAACCTCGCATCTCGACTTCTCTC 246
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Db 697 CGGCCCCAGCAGGGTGCACACGCGCGGCGAGTCTGCTGTTGGTGGTCTG 756
Qy 142 SerPheMetThrAnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 757 GCCTTCCTGCTGTACGGACGACCATCCTG-----AGCTGGAGTACCTCTCGGG 807
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpTrpPheAla 174
Db 808 GGCAGCTCCATCCCGAGGGCCATGCTATGCCAGTCTCTCACTGATGATCTCTC 867
Qy 175 LeuProThrSerLeuLeuGluPheLeuLeuProIleLeuLeuValAlaTrpPheSerAla 194
Db 868 ATCAGCGCTTCCACCTGGAGTCTTTAGGCCCTCTCTCAGCGTCACCTCTTTAACTC 927
Qy 195 HisIleTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 928 AGCATCTACTGTGAATCCTCAGAGCGCACCGCTCGGCTGGATGGGCTCGAGGCA 987
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 988 GCCGGCCCGAGCCCTCCGAGGCGCAGCCCTCACACCCCGCCCTGGCTGGTGG 1047
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 1048 GGCTGCTGGCAGAGGGGCACGGGAGGCCATG-----CGCTGCACAGTATGGG 1098
Qy 236 -----AlaThrLeu----- 238
Db 1099 GTGGTGTAGGCGCGGTAGGCGCTCAGCGCGGGGAGCGACCTCGGGGGTGGCGTGGG 1158
Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 1159 GCGGCTCGGTGGTTCACCACTCCAGCTCCGCGCAGCTCTCGAGGGGCATGAGAGG 1218
Qy 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTrpLysAsnSerAsnValIle 272
Db 1219 CCGGCG-----TCACTCAAGGGGGCTCCAGCGCTCGGCTCGGCTCGCTG 1269
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnGlnArgGluHis 292
Db 1270 GAGAGCGCATGAAGTGTCTCCAGAGCTTCACC-----CAGCGC 1311
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPhe 312
Db 1312 TTTGCGTGTCTCGGACAGAAAGTGCAGGCTGCTGGCTCTTGGCTCTTGGCTCTTT 1371
Qy 313 AlaIleCysTrpAlaProTrpSerLeuThrThrValIleTrpSerPheProGluArg 332
Db 1372 GGGCTCTGCTGGGCCCATACACGCTGTGATGATCATCCGGCGCGCTGC---CATGGC 1428
Qy 333 AsnLeuThrLysSerThrTrpTrpHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1429 CACTGCGTCCCTGACTACTGTGTACGAACCTCTTCTGGCTCTTGGCTCTTGGCT 1488
Qy 353 ValAsnProPheLeuTrpProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1489 GTCAACCTGTCTCTACCTCTGTGCCACACACAGCTTCCGCGGGCGCTTCCACAAGCTG 1548
Qy 373 LeuProValArgArgGlnSerThrProHisAsn 384
Db 1549 CTCTGCCCGCAGAGCTCAAAATCCAGCCCGCCACAGC 1584
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RESULT 13

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US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Alignment Scores:
Pred. No.: 9,76e-63 Length: 2665
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13
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US-10-626-398-10 (1-389) x US-09-949-016-5059 (1-2665)

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Qy 3 AlaAsnAsmSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 367 GCGCGGGCTTCTGGCAGCTCGACCGCGGTG-----CTGGCGCGCTCATGGCG 417
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 418 CTGCTCATCTGTCGACCGTGTGGGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
Qy 43 ArgAsnLeuArgHisArgSerAsnTrpPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 478 TCGAGCCTCCGCCACCCCAACAACTTCTCTCTCAACCTCGCATCTCCGATCTTCCTC 537
Qy 63 ValGlyAlaIleAlaIleProLeuTrpIleProSerSerLeuThr---TyrTrpThrSer 81
Db 538 GTGCGCGCTTCTGCATCCCACTGTATGATACCTACGTGCTGACAGCGCGCTGACCTTC 597
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTrpLeuLeuCysThrAlaSerVal 101
Db 598 GCGCGGGCGCTCTGCAAGCTGTGGCTAGTAGTACCTACCTGCTGTGCTGCTGCTGCTG 657
Qy 102 TyrAsnIleValLeuIleSerTrpAspArgTrpGlnSerValSerAsnAlaValTrpTyr 121
Db 658 TTCAACATCTGCTCATCAGTACGACCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 718 CGGCGCCAGCAGGGTGCACGCGCGGGCGAGTGGCGGAGATGCTGCTGGTGGTGGTGGT 777
Qy 142 SerPheMetThrAnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 778 GCCTTCCTGCTGTACGAGCAGCGACCATCTG-----AGCTGGAGTACCTCTCGGG 828
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpTrpPheAla 174
Db 829 GGCAGCTCCATCCCGAGGGCCATGCTATGCCAGTCTTCTCAAACTGGTACTCTCTC 888
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTrpPheSerAla 194
Db 889 ATCAGCGCTTCCACCTGGAGTCTTTAGCGCCCTCTCTCAGCGTCACTCTCTTTAACTC 948
Qy 195 HisIleTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 949 AGCATCTACTGTGAATCCTCAGAGCGCACCGCTCGGCTGGATGGGCTCGAGAGGCA 1008
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 1009 GCCGGCCCGAGGCCCTCTCCGAGGCGCCAGCCCTCACACCCCGCCCTGGCTGGTGG 1068
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
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Db 1069 GCCTGCTGGCAGAGGGGACGGGAGGCCATG-----CCGCTGCACAGGTATGGG 1119
Qy 236 -----AlaThrLeu----- 238
Db 1120 GTGGGTGAGCGCGCTAGCGCTGAGCGCGGGGAGGACCCCTCGGGGGTGGCGGTGGG 1179
Qy 239 -----ProAlaArgLysGluThrAlaSerLeuGlySerAspLys 252
Db 1180 GCGCGCTCGGTGGCTTACCCACCTCCAGCTCCGCGAGCTCCCTCGAGGGGCACTGAGAG 1239
Qy 253 SerArgArgLysSerSerLeuLeuProSerLeuAlaTyrLysAsnSerAsnValIle 272
Db 1240 CCGCGC-----TCACTCAAGAGGGGCTCCAAGCGTCCGCGCTCTCGGCTCACTG 1290
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1291 GAGAAGCGCATGATGCTCCAGAGCTTCACC-----CAGCGC 1332
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaLysLeuAlaLysPhe 312
Db 1333 TTTCGGCTGCTCCGGGAGCAGGAAGTGGCAGTCCGCTGGCGCTCATCTGAGCATCTTT 1392
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPheProGluArg 332
Db 1393 GGGCTCTGCTGGGCCCCATACAGCTGCTGATGATCATCCGGGCGGCTGC---CATGGC 1449
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1450 CACTGCGTCCCTGACTACTGTGTACGAACCTCTTCTGCTCTGCTGGGCAACTCGGCT 1509
Qy 353 VallanProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1510 GTCAACCTCGTCTTACCTCTGTGTGCCACACACAGCTTCGCGGGGCTTCACCAAGCTG 1569
Qy 373 LeuProValArgGlnSerThrProProHisAsn 384
Db 1570 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGC 1605
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RESULT 14

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US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 588593
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-08-985-090-1
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Alignment Scores:

Pred. No.:	9,91e-63	Length:	2689
Score:	689.50	Matches:	161
Percent Similarity:	53.5%	Conservative:	70
Best Local Similarity:	37.3%	Mismatches:	132
Query Match:	33.9%	Indels:	69
DB:	2	Gaps:	13

US-10-626-398-10 (1-389) x US-08-985-090-1 (1-2689)

```
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 366 GCGCGCGCTTCTCGGCAGCTGACACCGCGGTG-----CTGGCCGCGCTCATGGCG 416
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 417 CTGCTCATCTGCTGGGCACGCTGCTGGGCAACGCGTGGTGCATGCTGCGCTTCGTGGCCGAC 476
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 477 TCGAGCTTCCGCCACCCAGAACACTCTTCTCTGCTCAACCTCGCCCATCTCGACTCTCTC 536
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 537 GTGCGGCGCTTCTGCATCCCACTGATGATACCTAGCTGCTGACAGGCGCTGGACCTTC 596
Qy 82 GlyLysGlnAlaCysValPheTrpIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 597 GCGCGGGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACCTCTCTCTGCC 656
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 657 TTCAACATCGTGTCTCATGCTAGCAGCTACGACGCTCTCTGCTCGGTCAACCGAGCGGTCTCATAC 716
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 717 CGGCCCCAGCAGGCTGACACGCGCGGGCAGTGGCGAAGATGCTGCTGTGTGGTGTGCTG 776
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 777 GCCTTCTGCTGTACGGACCAACCATCTCTG-----AGCTGGGAGTACCTGTTCGGG 827
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpPheAla 174
Db 828 GGCAGCTCCATCCCGGAGGGCCACTGCTATGCCAGATTTCTTCTACAACTGTGTACTCTCTC 887
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 888 ATCAGCGGCTTCCACCTGGAGTCTTTACGCGCTTCTCTCAGCGTCACCTCTTTAACTCTC 947
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 948 AGCATCTACTGAACATCCAGAGGCGCACCGCCCTCCGCTCGGCTGGAGTGGGCTCGAGAGCA 1007
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 1008 GCCGCGCCCGAGCCCCCTCCCGAGGCGCAGCCCTCACACCCACCGCTGGGTGGTGG 1067
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 1068 GGCTGCTGGCAGAGGGGCGACGGGAGGCCATG-----CCGCTGCACAGGTATGGG 1118
```

```
Qy 236 -----AlaThrLeu----- 238
Db 1119 GTGGGTAGGCGCGCTAGGCGCTAGCGCGGAGGACCTTCGGGGTGGCGGTGGG 1178
Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 1179 GCGCGCTCCGTGGCTTCACCCACCTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGG 1238
Qy 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValle 272
Db 1239 CCGGCG-----TCACTCAAGAGGGGCTCCAAAGCGCTCGGCGTCTCGGCTCACTG 1289
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1290 GAGAGCGCATGAAGTGTCTCCAGAGCTTCACC-----CAGCGC 1331
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaLysLeuLeuAlaAlaPhe 312
Db 1332 TTTCGGCTGTCTCGGACAGGAAAGTGCCAAAGTCGTGGCGGTCATCGTGAGCATCTTT 1391
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1392 GGGCTGTGCTGGGCCCCATACACGCTGTGATGATCATTCGGCGCGCTGC---CATGGC 1448
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1449 CACTGCGTCCCTGACTACTGTGTAGAAACCTCTCTGGCTCTGTGGGCCAATCTCGCT 1508
Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1509 GTCAACCTGTCTTACCCTCTGTGCCACACACAGCTTCGCGCGGCTTCACCAAGCTG 1568
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1569 CTCTGCCCCAGAAAGCTCAAAATCCAGCCGCCACAGC 1604
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RESULT 15

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US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-09-165-543-1

Alignment Scores:
Pred. No.: 9,91e-63 Length: 2689
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: Gaps: 13

US-10-626-398-10 (1-389) x US-09-165-543-1 (1-2689)

Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 366 GCGCGCGGCTTCGGGAGGCTGACCGCGGTG-----CTGGCGCGGCTCATGGCG 416
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 417 CTGCTCATCGTGGCCACGGTGTGGCAACGCGCTGCTCATGCTGCGCTTCGTGGCGGAC 476
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 477 TCGAGCCTCCGCCACCCCAACAACTTCTCTCGCTCAACCTCGCCATCTCGACTTCCTC 536
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 537 GTGCGCGCCTTCTGCATCCCATGATGATGATGATGATGATGATGATGATGATGATGATG 596
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrIleLeuLeuCysThrAlaSerVal 101
Db 597 GCGCGCGGCTCTGCAAGCTGTGGTAGTAGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 656
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 657 TTCAACATCGTGTCTCATCAGTACGACCGCTTCTCTGCGGTGATGCTGCTGGTGTGGTGTG 716
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 717 CCGGCCCCAGCAGGTGACACGCGCGGCGAGTGGGAGATGCTGCTGGTGTGGGTGCTG 776
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 777 GCCTTCTGCTGTACGACGACGACCATCTG-----AGCTGGAGTACCTGTCCGGG 827
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTyrTrpPheAla 174
Db 828 GGCAGCTCCATCCCGGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGTGTACTCTCTC 887
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 888 ATCAGCGCTTCCACCTGGAGTTCTTTACGCCCTTCTCTCAGCGTCACCTCTTTAACTCTC 947
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 948 AGCATCTACCTGAACATCCAGAGCGCACCGCGCTCCGCTGGATGGGTGCGGAGGCA 1007
Qy 211 SerHisProValLeuProSerAspSerSerSerSer----- 222
Db 1008 GCCGCGCCCGAGCGCCCTCCGAGGCCACGCCCTCACACCCCGCTGGGTGTGGTGG 1067
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 1068 GGCTGTCTGGCAGAGGGGCGACGGGAGGCCATG-----CCGCTGCACAGGTATGGG 1118
Qy 236 -----AlaThrLeu----- 238
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Db 1179 GCGCGCTCGTGGCTTTCACCCACCTCCAGCTCGGCAGCTCCTCGAGGGGCACTGAGAGG 1238
QY 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
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Db 1290 GAGAGCGCATGAGATGTTGCCAGAGCTTCACC-----CAGCGC 1331
QY 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaLaphe 312
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QY 313 AlaIleCysTIPAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
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GenCore version 5.1.7
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Run on: April 29, 2006, 23:57:38 ; Search time 3185 Seconds
(without alignments)
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Perfect score: 2036
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Fgapop 6.0 , Fgapext 7.0
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Total number of hits satisfying chosen parameters: 19587084

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Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2025	99.5	1170	9	US-10-626-126-7
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4	1308.5	64.3	1170	9	US-10-488-421-7
5	1308.5	64.3	1173	3	US-09-812-216-1
6	1308.5	64.3	1173	3	US-09-910-411-1
7	1308.5	64.3	1173	3	US-09-875-076-13
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Sequence 7, Appli					Sequence 7, Appli
Sequence 1, Appli					Sequence 1, Appli
Sequence 13, Appli					Sequence 13, Appli

8	1308.5	64.3	1173	3	US-09-876-252-13	Sequence 13, Appli
9	1308.5	64.3	1173	5	US-10-052-193-1	Sequence 1, Appli
10	1308.5	64.3	1173	6	US-10-272-983-13	Sequence 13, Appli
11	1308.5	64.3	1173	6	US-10-354-769-1	Sequence 1, Appli
12	1308.5	64.3	1173	6	US-10-393-807-13	Sequence 13, Appli
13	1308.5	64.3	1173	7	US-10-417-820A-13	Sequence 13, Appli
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15	1308.5	64.3	1173	7	US-10-723-955-13	Sequence 13, Appli
16	1308.5	64.3	1173	7	US-10-782-596-13	Sequence 13, Appli
17	1308.5	64.3	1173	7	US-10-737-619-1	Sequence 1, Appli
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21	1308.5	64.3	1173	9	US-10-626-398-1	Sequence 1, Appli
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24	1308.5	64.3	1300	3	US-09-852-165-1	Sequence 1, Appli
25	1308.5	64.3	1300	5	US-10-696-673-1	Sequence 1, Appli
26	1308.5	64.3	3689	5	US-10-225-567A-628	Sequence 628, App
27	1308.5	64.3	3689	8	US-10-684-206-19	Sequence 19, Appli
28	1308.5	64.3	3689	9	US-10-756-149-32	Sequence 32, Appli
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30	1306.5	64.2	1265	6	US-10-290-078-25	Sequence 25, Appli
31	1306.5	64.2	1265	9	US-10-488-421-5	Sequence 5, Appli
32	1244	61.1	1176	8	US-10-626-445-5	Sequence 5, Appli
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36	1235.5	60.7	1176	9	US-10-626-126-6	Sequence 6, Appli
37	1235.5	60.7	1176	9	US-10-626-398-6	Sequence 6, Appli
38	1166	57.3	1166	9	US-10-488-421-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-10-626-445-7
; Sequence 7, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-445-7

Alignment Scores:
Pred. No.: 4.67e-219 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.7% Conservativeness: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 8 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-445-7 (1-1170)

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Db 1 ATGTGGCAATAACAGTACATGCCCTTAACATCAATTAATAATTTCTTTGACATTTTAA 60

Qy 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAnValValIleLeuAlaPheIle 40
Db 61 ATGTCTTTACGTAGCTATTGCTATATGTTAGCAATGTCGGTCAATTTTAGCTTTTATT 120

Qy 41 ValAspArgAnLeuArgHisArgSerAsnTyrPhePheLeuAnLeuAlaIleAlaAsp 60
Db 121 GTGACAGAAATCTAGACATCGAAGTAATTTACTTTTCTTAACCTGGCCATTGCGAC 180

Qy 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTTCTTTGGGTGGCAATTTGCAATTCCTCTGTACATACCTTCTCGCTGACTTACTGGACT 240

Qy 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
Db 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCAATTTACTGACTATCTTTTATGTACGACTCT 300

Qy 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120
Db 301 GTGTATAATATTTCTCATCAGTACGATCGTACCACTGAGTCTCAATGCCGTGGG 360

Qy 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140
Db 361 TATGAGCTCAGCACTCTGGCACCTTGGCACTTGGCAATTTGCTACAGATGGTGGCTTTGGATA 420

Qy 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 421 TTTCTCTTCATGACAAATGGGCGGATGATTTCTGATTTTCTGAGACTCTTGGCAATGACT 480

Qy 161 ThrGluCysGluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuLeu 180
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Qy 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db 541 GAAATTCCTGATCCCATCTGTTAGTTGCTATTTTCTGAGCGGCAATATTTTCTGGAGCTG 600

Qy 201 TrpLysArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
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Qy 241 ArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
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Db 841 CACTCAGATTTCTGGCTCTTCAGCAAGGGAAACATTCGAATTTTTCAGAGCCAGGAAA 900

Qy 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer 320
Db 901 TTAGCCAAAGTCACTGGCCCATCTCTTAGCAGCTTTTGGCCATTTGCTGGCTCCATTTCA 960

Qy 321 LeuThrThrValIleTyrSerPhePheProGluArgAnLeuThrLysSerThrTrpTrp 340
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Qy 341 HisThrAlaPheTrpLeuGlnTrpPheAnSerPheValAsnProPheLeuTyrProLeu 360
Db 1021 CATACTGCCCTTTGGCTCCAGTGGTTCAATTCCTTTGTTTAAATCCCTTTTGTATCATTTG 1080

Qy 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThr 380
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RESULT 2
US-10-626-126-7
; Sequence 7, Application US/10626126
; Publication No. US20050074770A1
GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changliu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-126-7

Alignment Scores:
Pred. No.: 4,67e-219 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 9 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-126-7 (1-1170)

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Qy 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
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Qy 41 ValAspArgAnLeuArgHisArgSerAsnTyrPhePheLeuAnLeuAlaIleAlaAsp 60
Db 121 GTGACAGAAATCTTAGACATCGAAGTAATTTACTTTTCTTAACCTGGCCATTGCGAC 180

Qy 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTTCTTTGGGTGGCAATTTGCAATTCCTCTGTACATACCTTCTCTCGCTGACTTACTGGACT 240

Qy 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
Db 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCAATTTACTGACTATCTTTTATGTACAGCACT 300

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Qy 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140
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Qy 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
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QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSer 320
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QY 321 LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyr 340
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QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
Db 1021 CATATCGCTTTTGGCTCCAGTGGTTCATTTCTTTGTATTCCTTTTGTATTCATTTG 1080
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Db 1081 TGTCAAACGTTTTTCAGAGGCTTCTCTGAAATATCTCTGTGGAAGGCAATCCACG 1140
QY 381 ProProHisAsnArgSerIleSerThr 398
Db 1141 CCACCACACACCGCTCAATATCCACT 1167
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RESULT 3

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US-10-626-398-7
; Sequence 7, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-398-7
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Alignment Scores:

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Pred. No.: 4,67e-219 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 9 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-398-7 (1-1170)

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Db 1 ATGTGGCAATTAACAGTACAAATCGCCTTAACATCAATTAATAATTTCTTTGACATTTTAA 60
QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAlaPheIle 40
Db 61 ATGTCTTTTACTAGCTTATTTGCTTATAATGTATGGCAATGTGGTGCATTTTACTTTTATT 120
QY 41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAsp 60
Db 121 GTGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTTTAACTTGGCCATTTGCAGAC 180
QY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTTCTTTGGGTGCAATTTGCAATTTCTCTGTACATACCTTCTCGCTGACTTACTGGACT 240
QY 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
Db 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTATACACATCT 300
QY 101 ValTyrAniIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120
Db 301 GTGTATATATTTGCTCTCATCAGCTACGATCGCTACCGAGTCACTCAATATGCCGTGTGG 360
QY 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140
Db 361 TATAGAGCTCAGCACTCTGGCACCTTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420
QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 421 TTTCTCTTTCATGACAAATATGGGCGCATGATTTCTGATTTTCAGACTCTCTGGCAGATAGCACT 480
QY 161 ThrGluCysGluProGlyPheLeuLysTyrTrpPheAlaLeuProThrSerLeuLeu 180
Db 481 ACAGATGTGAACCTGGATTTTAAAAAGTGGTACTTTGGCTCTCCCTACATCATTTATG 540
QY 181 GluPheLeuLeuProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db 541 GAATTCCTGATCCCATCTTGTTAGTTGCTTATTTTCAGCGCCCATATTTTACTGGAGCCTG 600
QY 201 TrpLysArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
Db 601 TGGAAAGCGAGAGAACTGAGCAGGTGGCTCTCAGCCACCTGTACTCTCCCTCTGACTCTTCC 660
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
Db 661 AGCAGTGACCGAGACACTCTCTGCGAGACAGGACCCCGATTCAAGGGCGACTCTTCCGACA 720
QY 241 ArgLysGluThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
Db 721 CGGAAGAAGAACACTCGCTCTCTGGTTCAGCAAGTCAAGGAGAAAGAGCAGTCTCTTG 780
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Db 781 TTTTCCATAAGAGCCTTACAGAACAGCAATGTGATCGCTTCCCAAAATGGGCTTCTCTCC 840
QY 281 HisSerAspSerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLys 300
Db 841 CACTCAGATTCCTCGGCTCTTTCAGCAAGGAGGAAACATATCGAACTTTTCAGAGCCAGGAAA 900
QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSer 320
Db 901 TTAGCAAGTCTCTGGCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATTTCA 960
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Qy 321 LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrIlysSerThrTrpTyr 340
Db 961 CTGACTACAGTATCTACTCATTTTCTCTGAAGGAACCTTGACTAAATCAACCTGGTAC 1020

Qy 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
Db 1021 CATACTGCTTTTGGCTCCAGTGGTTCAATTCCTTTGTATATCCCTTTTGTATCCATTG 1080

Qy 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThr 380
Db 1081 TGTCAAAAGCTTTTCAGAGGCTTTCTGAAATACCTCTCTGTGAGAGGCAATCCACG 1140

Qy 381 ProProHisAsnArgSerIleSerThr 389
Db 1141 CCACCACACACCGCTCAATATCCACT 1167

RESULT 4
US-10-488-421-7
; Sequence 7, Application US/10488421
; Publication No. US20050239065A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc. [US/US]
; APPLICANT: Gallagher, Michael J.
; APPLICANT: Yates, Stephen L.
; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES
; FILE REFERENCE: 1367-13335W001
; CURRENT APPLICATION NUMBER: US/10/488,421
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US 60/316,762
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/332,697
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent
; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.
; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequence
; OTHER INFORMATION: only
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462
; OTHER INFORMATION: are AAG and 988 is C
US-10-488-421-7

Alignment Scores:
Pred. No.: 1,17e-137 Length: 1170
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: Gaps: 9
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US-10-626-398-10 (1-389) x US-10-488-421-7 (1-1170)
Qy 5 AsnSerThrIleAlaLeuThr----SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCATTTTATGTCTCTTA 72

Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTCTATAATAGCTAGGAATGCTTTGGTCATTTTAGCTTTTGTGGTGACAA 132

Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
Db 133 AACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGCCATCTCTGACTTCTTGTG 192

Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTTCTTTGTATACCTCCCTCACAGCTGTTCGAATGGGATTTTGGAAAG 252

Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAAATCTGTGTATTTTGGCTCACTACTGATGATCGATCTCAAGTCTGTGTCTTATATAC 312

Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
Db 313 ATTGTCTCATCAGCTATGATCGATCTGCTAGTCTCAATGCTGTGTCTTATAGAACT 372

Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATATGGGGTCTTGAAGATTGTACTCTGATGTTGGCCGTTTGGGTGCTGGCCTTC 432

Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163
Db 433 TTAGTGAATGGGCAATGATTCTAGTTTCAGAGTCTTGGAGAGGATGAAGGTAGTGAATG 492

Qy 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGTTACATCTCTGCCATCACATCATCTTGGAAATCGTG 552

Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATTGGAGCCTGTGGAAGCGT 612

Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGCTCT---GTCCTCTCCACATC 669

Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGGACACTCATTTACAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGTCATCGACAGAA 729

Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerSerLeuLeuProSerIle 263
Db 730 GTTCTGTCATCTTTTCATTTCAGAGACAGAGGAGAAAGAGTAGTCTCATGTTTTCCTCA 789

Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACAAATTCCTTCCAAATGGGTCTCTTCTCCCATCAGAT 849

Qy 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGTCTTTCACCAAGGGACATCTTGAACCTGTAGAGCCAGGAGATTAGCCAAAG 909

Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerIleuThrThr 323
Db 910 TCACCTGGCCATCTCTTAGGGGTTTCTGTGCTGGCTGCCATATATCTCTGTGTACA 969

Qy 324 VallIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
Db 970 ATTGTCTTTTCAATTTATTTCTCTCAGCAACAGGCTCTCAATTCAGTTGGTATAGAAATGCA 1029

Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
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Db 1030 TTTTGGCTTCAGTGGTTCAATCTTTTGTCAATCTCTTTTGTATCCATTTGTGTACCAATGTGTGCACAA 1089

Qy 364 ArgPheGlnIleAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382

Db 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAGCAACCTCTACCATCACAA 1149

Qy 383 HisAsnArgSerIleSerThr 389

Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 5

US-09-812-216-1

; Sequence 1, Application US/09812216

; Patent No. US20020098539A1

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monama, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

; APPLICANT: Wang, Suke

; TITLE OF INVENTION: Histamine receptor

; FILE REFERENCE: CN01069

; CURRENT APPLICATION NUMBER: US/09/812,216

; PRIOR FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 09/414,010

; PRIOR FILING DATE: 1999-10-07

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-812-216-1

Alignment Scores:

Pred. No.:	1.18e-137	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.5%	Conservative:	48
Best Local Similarity:	65.1%	Mismatches:	84
Query Match:	64.3%	Indels:	3
DB:	3	Gaps:	3

US-10-626-398-10 (1-389) x US-09-812-216-1 (1-1173)

Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23

Db 13 AATAGCACAAATCAATTTATCACTAGCACTCGTGTACTTTAGCATTTTATGTCCTTA 72

Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43

Db 73 GTAGCTTTTGTATAATGCTAGGAATGCTTTGGTCAATTTTAGCTTTTGTGTGCACAA 132

Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63

Db 133 AACCTTAGACATCGAAGTAGTATTTTCTTAATCTTGGCCATCTCGACTTCTTGTG 192

Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerLeuThrTyrTrpThrSerGlyLys 83

Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTACAGCGTTCGATGGATTTGGAAAG 252

Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTrpAsn 103

Db 253 GAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTATGACAGCATCTGTATATAAC 312

Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTrpArgAla 123

Db 313 ATTGTCTCATCAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372

Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143

Db 373 CAACATCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCCGTTTGGGTGTCGGCCCTC 432

Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163

Db 433 TTATGGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAGAGTGAAGGTAGTGAATGT 492

Qy 164 GluProGlyPheLeuLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183

Db 493 GNACTGGATTTTTTTCGAAATGGTACATCTTCGCATCACATCATTTCTTGGAAATTCGTG 552

Qy 184 IleProIleLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203

Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATAATTTATTCGAGCTGTGGAAGCGT 612

Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223

Db 613 GATCATCTCAGTAGGTGCCAAAGCCATCTCGACTGACTGCT--GTCTCTTCCAAATC 669

Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243

Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAGAGAGATCTCTTTCGCATCGACAGNA 729

Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263

Db 730 GTTCCTGCATCTCTTTCATTCAGAGAGACAGAGAGAGTAGTCTCATGTTTCTCTCA 789

Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283

Db 790 AGAACCAAGATGAATAGCAATACATTCCTTCCAAATGGGTCTCTTCTCCCAATCAGAT 849

Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303

Db 850 TCTGTAGCTCTTCACCAAGGGAACATGTTGAACTCTTAGAGCCAGAGATTAGCCAG 909

Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323

Db 910 TCAGTGGCCATCTCTTAGGGGTTTTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 969

Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343

Db 970 ATTGTCTCTTTCATTTTATTCCTTCAGCACAGGTCCTAAATCAGTTTGTATAGAAATTGCA 1029

Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363

Db 1030 TTTTGGCTTCAGTGGTTCATCTCTTGTCAATCTCTTTGTATCCCAATTTGTGTGCACAG 1089

Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382

Db 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAGCAACCTCTACCATCACAA 1149

Qy 383 HisAsnArgSerIleSerThr 389

Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 6

US-09-910-411-1

; Sequence 1, Application US/09910411

; Patent No. US20020137054A1

; GENERAL INFORMATION:

; APPLICANT: Bergsma, Derk

; APPLICANT: Fitzgerald, Laura

; APPLICANT: Li, Xiaotong

; APPLICANT: Michalovich, David

; APPLICANT: Zhu, Yuan

; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor

; FILE REFERENCE: GP70655-2C1

; CURRENT APPLICATION NUMBER: US/09/910,411

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: 09/693,761

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 09/497,790

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/431,898

; PRIOR FILING DATE: 1999-11-02

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Alignment Scores:
Pred. No.:      1.18e-137      Length:      1173
Score:          1308.50      Matches:      252
Percent Similarity: 77.5%      Conservative: 48
Best Local Similarity: 65.1%      Mismatches: 84
Query Match:      64.3%      Indels:      3
DB:              3          Gaps:      3

US-10-626-398-10 (1-389) x US-09-910-411-1 (1-1173)

Qy 5 AasnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTTTATGTCCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGTCTAATCTAGGAATGCTTTGTGTCATTTTGTGCTTTGTGGTGACAA 132
Qy 44 AasnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGGCCATCTCTGACTTCTTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCGAATGGATTTTGGAAAG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrIleLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAATCTGTGTATTTTGGCTACTACTGACTATCTGTTATGTATGACGACATCTGTATATAC 312
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTrpArgAla 123
Db 313 ATTTGCTCATCAGCATGATGATGATCTGTCAGTCTCAATGCTGTGTCTTATAGAACT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
Db 373 CAACATACCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCGGTGTGGGTGCGCCCTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAAGTAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuGluPheLeu 183
Db 493 GAACTGGATTTTTCGGAATGGTACATCCTTGGCATCACATCATCTTGGAAATTCGTG 552
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCACTTAGTCGCTTATTTCAACATGAATATTTATTTGGAGCCTGTGGAAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCGAAAGCCATCTCGACTGACTGCT---GTCTCTTCCAACTC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGGATCTCTTCTGTCATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCTCTGCATCTCTTTCATTCAGAGACAGAGAGAGAGTAGTCTCATGTTTTCCTCA 789
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACAAATTGCTTCCAAATGGGTCTCTTCCCAATCAGAT 849
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284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaAargLysLeuAlaLys 303
850 TCTGTAGCTCTTCCACAAAGGAAACATGTTGAAGTCTTGTAGCCAGGAGATTAGCCAG 909
304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 323
910 TCACTGGCCATTTCTTTAGGGGTTTTTGTGTTTGTGCTGGCTCCATATCTCTGTTTCA 969
324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTrpHisThrAla 343
970 ATTGTCTCTTTCAATTTATTTCTCAGCAACAGGCTCTTAATCAGTTTGGTATAGAAATTGCA 1029
344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
1030 TTTTGGCTTCAGTGGTTCAATTTCTTTGTCAATCTCTTTGTATCCATTTGTGTGTCACAAG 1089
364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro---Pro 382
1090 CGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAAGCAACCTCTACCATCACA 1149
383 HisAsnArgSerIleSerThr 389
1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 7
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
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Qy	244	ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle	263
Db	730	GTTCCTGCATCCTTTTCATTCAGAGACACAGAGAGAAAGTAGTCTCTCATGTTTTCTCTCA	789
Qy	264	ArgAlaTyrllysAsnSerAsnValIleAlaSerIysMetCglyPheLeuSerHisSerAsp	283
Db	790	AGAACCAAGATGATAGCAATACAAATGCCTTCACAAATGGGTCTCTTCTCCCAATCAGAT	849
Qy	284	SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys	303
Db	850	TCTGTAGCTCTTCACCAAGGGAACATGTTGAACTGCTTAGAGCCAGGAGATAGCCCAAG	909
Qy	304	SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr	323
Db	910	TCACGTGCCATTCTCTTAGGGGTTTTTGTCTGTTTGTCTGGGCTCCATATTCCTGTTTCA	969
Qy	324	ValIleTyrSerPhePheProGluArgAsnLeuThrIlysSerThrTrpTyrHisThrAla	343
Db	970	ATTGTCTCTTCATTTATTATTCCTCAGCAACAGGTCCTAAATCAGTTGGTATAGAAATGCA	1029
Qy	344	PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys	363
Db	1030	TTTTGGCTTCAGTGGTTCATTCCTTTGTGCATCCTCTTTTGTATCCATGTGTGCACAG	1089
Qy	364	ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---	382
Db	1090	CGCTTTCAAAGGCTTCTTGAAATATTTTGTATAAAAAAGCAACCTCTTACCATCAAA	1149
Qy	383	HisAsnArgSerIleSerThr	389
Db	1150	CACAGTCGGTCAGTATCTTCT	1170

RESULT 8

US-09-876-252-13

Sequence 13, Application US/09876252

Publication No. US20030018182A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Lehmann-Bruinsma, Karin

APPLICANT: Chalmers, Derek T.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Lin, I-Lin

APPLICANT: Dang, Huong T.

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Cou

FILE REFERENCE: AREN-0054

CURRENT APPLICATION NUMBER: US/09/876,252

CURRENT FILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: 09/416,760

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/110,060

PRIOR FILING DATE: 1998-11-27

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,852

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/109,213

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/123,944

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,945

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,948

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,951

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

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/ PRIOR APPLICATION NUMBER: 60/152,524
/ PRIOR FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: 60/151,114
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ NUMBER OF SEQ ID NOS: 146
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-876-252-13

Alignment Scores:
Pred. No.: 1,18e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3

US-10-626-398-10 (1-389) x US-09-876-252-13 (1-1173)

QY 5 AnSerThrIleAlaLeuThr---SerIleLysLeuSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAAATCAATTTATCAAGCACTCGGTGTACTTTAGCACTTTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCATTTTAGCTTTTGTGGACAAA 132
QY 44 AnLeuArgHisArgSerAenTyrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATATTTTCTTAACCTGGCCATCTCTGACTTCTTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTTCACACGCTGTTCGAATGGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuLeuThrAspTyrLeuLeuCysThrAlaSerValTyrAen 103
Db 253 GAAATCTGTGATTTTGGCTCACTGACTACTCTGTTATGTATACAGCACTCTGTATATAAC 312
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QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaValTyrTrpArgAla 123
Db 313 ATTGTCCTCATCAGCTATGATGATCTGTCAGTCTCAAAATGCTGTGTCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATCTGGGGCTTTGAAGATTGTTACTCTGATGGTGGCGCTTTGGTGTGTCGCCCTTC 432
QY 144 MetThrAenGlyProMetIleLeuIleSerAspSerTrpGlnAenSerThrTrpGluCys 163
Db 433 TTAGTGAATGGGCAATGATTCTAGTTTCAGAGTCTTGGAAAGGATGAAGGTGAATGT 492
QY 164 GluProGlyPheLeuLysLysTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTACATCTCTGCCATCACATCATTTCTTGGAAATTCGTG 552
QY 184 IleProIleLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATTTGGAGCTGTGGAAGCGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCCAAAGCCATCTCTGACTGCTCT--GTCTCTTCCAAATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAGGAGATCTCTTTCGCATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCCTGCATCTCTTTCATTCAGAGACAGAGGAGAGAGTAGTCTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAenSerAenValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACAAATTCCTTCCAAAATGGGTCTCTTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCACCAAGGAAACATGTTGAACTGCTTAGACGACGAGGATTAGCCAAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACCTGGCCATCTCTTAGGGGTTTTTGTCTGTCTGGCTCCATATTTCTGTGTCA 969
QY 324 ValIleTyrSerPhePheProGluArgAenLeuThrLysSerThrTrpTyrHisThrAla 343
Db 970 ATTGTCTTTCATTTTATTCCTCAGCAACAGGTCTCTAAATCAGTTTGTATAGAATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAenSerPheValAenProPheLeuTyrProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTTGTATCCATTTGTGTACAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAGGCTTTCTTGAATAATATTTTGTATAAAAAAGCAACCTCTACCAACAA 1149
QY 383 HisAenArgSerIleSerThr 389
Db 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 9
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1

Alignment Scores:
Pred. No.:      1.18e-137      Length:      1173
Score:          1308.50      Matches:      252
Percent Similarity: 77.5%      Conservative: 48
Best Local Similarity: 65.1%      Mismatches: 84
Query Match:      64.3%      Indels:      3
DB:              5          Gaps:      3

US-10-626-398-10 (1-389) x US-10-052-193-1 (1-1173)

QY 5 AenSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCACAATCAATTAATCATAGCACTCGTGTTACTTTAGCAATTTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGCTATAATGCTAGAAATGCTTTGGTCAITTTAGCTTTTGTGGTGCAAA 132
QY 44 AenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATATTTTCTTAACCTGGCCATCTCTGACTCTCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
DB 193 GGTGTGATCTCCATTCCTTTGTACATCCCTCACGCTGTTTCGAATGGGATTTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAAATCTGTGATTTTGGCTCACTACTGATCTATCTGTTATGTACAGCATCTGTATATAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrPyrArgAla 123
DB 313 ATTGTCTCATCAGCTATGATCGATACCTGTCTCAGTCTCAAAATGCTGTCTTATAGAAT 372
QY 124 GlnHisSerGlyThrTrpIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
DB 373 CAACATCTGGGCTTCAAGATTTTACTCTGATGGTGGCGGTTGGTGTGCGCCCTC 432
QY 144 MetThrAenGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
DB 433 TTAGTGATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAAGTAGTGAATGT 492
QY 164 GluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 493 GAACCTGGATTTTTCGGAATGGTATCATCTCTGCAATCATCATCATCTTCTGGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpIleArg 203
DB 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATTTGAGGCTCTGGAAGCGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGTGCCAAAGCCATCTGACATGACTGTCT---GTCTCTTCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTTTTCTGTCATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCCTGTCATCTTTCATCTCAGAGAGACAGAGAGAAAGAGTAGTCTCATCTTTCTCTCA 789
QY 264 ArgAlaTyrLysAenSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCATAACAATTCCTTCCAAATGGGTTCCTTCTCCCAATCAGAT 849

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QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTCCACAAAGGGAACATGTTGAAGTCTTAGAGCCAGAGATTAGCCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
DB 910 TCACGTGGCCATCTCTTAGGGGTTTGTCTGTGGCTCCCATATCTCTCTGTTCCACA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
DB 970 ATTTGCTCTTTCATTTTATTTCTCTCAGCAACACAGGTCTCTAAATCAGTTTGTGTAGAAATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAenProPheLeuTyrProLeuCysHisLys 363
DB 1030 TTTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTATATCCATTTGTGTCAAAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CGCTTTCAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAACCTCTACCATCACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTGGTCTAGTATCTTCT 1170

RESULT 10
US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Alignment Scores:
Pred. No.:      1.18e-137      Length:      1173
Score:          1308.50      Matches:      252
Percent Similarity: 77.5%      Conservative: 48
Best Local Similarity: 65.1%      Mismatches: 84
Query Match:      64.3%      Indels:      3

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DB: 6 Gaps: 3

US-10-626-398-10 (1-389) x US-10-272-983-13 (1-1173)

Qy 5 AnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAAAATCAATATATCAATCAAGCACTCGTGTTACTTTAGCAATTTTATGTCCTTA 72

Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTAATAGCTAGGAATGCTTTGGTCAATTTTAGCTTTTGTGGTGACAAA 132

Qy 44 AnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATATTTTCTTAACCTGGCCATCTCTGACTCTCTTTGTG 192

Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTATCCCTCACAGCTGTTCGAATGGATTTGGAAAG 252

Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATAAC 312

Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
Db 313 ATTGTCTCATCAGCTATGATGATACCTGTCAGTCTCAATGCTGTGTCTTTATAGAAT 372

Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATATGGGGTCTTGAAGATTTACTCTGATGGTGGCCGTTTGGGTCTGCGCTTC 432

Qy 144 MetThrAnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGATGGCCAAATGATTTCTAGTTTCAGAGCTTGGAGGATGAAGTAGTGAATGT 492

Qy 164 GluProGlyPheLeuLysIleTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTATCATCTTGCATCATCATCTTCTTGGAAATTCGTG 552

Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGATATTTATTTGGAGCTGTGGAGCGT 612

Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGTGCCAAAGCATCTCTGGACTGACTGCT---GTCTCTTCCAACATC 669

Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGCACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGTCATCGACAGA 729

Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCTCGATCTCTTTCATTCAGAGGACAGAGGAGAGAGTAGTCTCATGTTTTCCTCA 789

Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATCATAGCATATACATATGCTTCCAAATGGGTCTCTTCTCCCAATCAGAT 849

Qy 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCCACAAAGGAAACATGTTGAATGCTTAGAGCCAGGAGATTAGCCAA 909

Qy 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACATGGCCATCTCTTATGGGGTTTGTGTGTGTGCTGGGCTCCATATCTCTGTTCACA 969

Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
Db 970 ATGTGCTTTTCATTTTATCTCTCAGCAACAGGTCCTAAATCAGTTTGGTATAGAATTGCA 1029

Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363

Db 1030 TTTTGGCTTCAGTGGTTCATTTCTTTGTCAATCTCTTTGTCAATCTCTTTTGTATCCATTTGTGTCAAG 1089

Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAGGCTTTCTTTGAAAATATTTTGTATATAAAAGCAACCTCTACCATCAAA 1149

Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACATCGGTTCAGTATCTTCT 1170

RESULT 11

US-10-354-769-1

; Sequence 1, Application US/10354769

; Publication No. US20030149242A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc.

; APPLICANT: O'Reilly, Mark A.

; APPLICANT: Peter. Beate

; TITLE OF INVENTION: NOVEL POLYPEPTIDE

; FILE REFERENCE: PC10373B

; CURRENT APPLICATION NUMBER: US/10/354,769

; CURRENT FILING DATE: 2003-01-30

; PRIOR APPLICATION NUMBER: US 09/698,801

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/211,243

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: GB 9925641.4

; PRIOR FILING DATE: 1999-10-29

; PRIOR APPLICATION NUMBER: GB 0009973.9

; PRIOR FILING DATE: 2000-04-20

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-354-769-1

Alignment Scores:

Pred. No.:	1.18e-137	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.5%	Conservative:	48
Best Local Similarity:	65.1%	Mismatches:	84
Query Match:	64.3%	Indels:	3
DB:	6	Gaps:	3

US-10-626-398-10 (1-389) x US-10-354-769-1 (1-1173)

Qy 5 AnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAAAATCAATATATCAATCAAGCACTCGTGTTACTTTAGCAATTTTATGTCCTTA 72

Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTAATAGCTAGGAATGCTTTGGTCAATTTTAGCTTTTGTGGTGACAAA 132

Qy 44 AnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATATTTTCTTAACCTGGCCATCTCTGACTCTCTTTGTG 192

Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTATCCCTCACAGCTGTTCGAATGGATTTGGAAAG 252

Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATAAC 312

Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
Db 313 ATTGTCTCATCAGCTATGATGATCAGTCTCAATGCTGTGTCTTTATAGAAT 372

Qy	124	GlnHisSerGlyThrTrpIysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe	143
Db	373	CAACATATCTGGGGTCTTGAAGATTCTTACTCTGATGGTGGCGGTATGGGTGCTGGCCCTTC	432
Qy	144	MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys	163
Db	433	TTAGTGAATGGCCCATGATTTCTAGTTTCAGAGTCTTGGAGGATGAAGAGTAGTAGTAATGT	492
Qy	164	GluProGlyPheLeuLysTrpTrpPheAlaLeuProThrSerLeuLeuGluPheLeu	183
Db	493	GAACCTGGATTTTTTCGGAATGGTACATCTCTTGGCATCATCATCTTCTGGAAATTCGTG	552
Qy	184	IleProIleLeuLeuValAlaTrpPheSerAlaHisIleIleTrpSerLeuTrpIysArg	203
Db	553	ATCCAGTCATCTTAGTCGCCTATTATTCAACATGAATATTATTGGAGCTCTGTGAAGCGT	612
Qy	204	GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp	223
Db	613	GATCATCTCAGTAGGTGCCAAGCCATCTCGAGCTGACTGCT--GTCCTCTCCACATC	669
Qy	224	HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu	243
Db	670	TGTGGACATCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGTCATCGACAA	729
Qy	244	ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle	263
Db	730	GTTCTGTGATCTCTTCAATCAGAGAGCAGAGGAGAAAGAGTAGTCTCATCTTTTCTCTCA	789
Qy	264	ArgAlaTrpLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283
Db	790	AGAACCAAGATGAATAGCAATACAAATGCCTTCCAATGGGTCTCTCTCCATCATCAT	849
Qy	284	SerLeuAlaLeuGlnArgGluHisIleGluIleuPheArgAlaArgLysLeuAlaLys	303
Db	850	TCTGTAGCTCTTCCACCAGGGAACATGTTCAACTGCTTAGAGCCAGAGATTAGCCAAG	909
Qy	304	SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysGlnTrpAlaProTyrSerLeuThr	323
Db	910	TCATCGGCCATCTCTTAGGGGTTTTGCTGTTTTGCTGGGCTCCATATTCTCTGTTCA	969
Qy	324	ValIleTrpSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla	343
Db	970	ATTGTCCTTTCATTTTATCTCTCAGCAACAGGTCTTAATCAGTTTGGTATAGAAATGCA	1029
Qy	344	PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys	363
Db	1030	TTTTGGCTTCAGTGGTTCAATTCCTTTTGTCAATCTCTTTTGTATCCATTGTGTCAAG	1089
Qy	364	ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro--Pro	382
Db	1090	CGCTTTCAAAAGGCTTTCTTGAAATATTTTGTATAAAGCAACCTCTACCATCAAA	1149
Qy	383	HisAsnArgSerIleSerThr	389
Db	1150	CACAGTCGGTCAGTATCTTCT	1170

RESULT 12
US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20

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; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

Alignment Scores:
Pred. No.: 1,188-137
Score: 1308.50
Percent Similarity: 77.5%
Best Local Similarity: 65.1%
Query Match: 64.3%
DB: 6
Indels: 3
Gaps: 3
Matches: 252
Conservative: 84
Indels: 84
Gaps: 3

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US-10-626-398-10 (1-389) x US-10-393-807-13 (1-1173)

Qy	5	AsnSerThrIleAlaLeuThr---	SerIleLysIleSerLeuThrPheLeuMetSerLeu	23
Db	13	AATAGCACAACTTATCATCATAAGCACTCGTGTTACTTTAGCACTTTTTATGTCCTTA	72	
Qy	24	LeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAlaPheIleValAspArg	43	
Db	73	GTAGCTTTGGTCTATAAATGCTAGGAATGCTTTGGTCATTTTTAGCTTTTGGTGGACAAA	132	
Qy	44	AsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleAlaAspPhePheVal	63	
Db	133	AACCTTAGACATCGAAGTAGTTATTTTTTCTTAACCTTGGCCATCTCGACTCTTTGTG	192	
Qy	64	GlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrTriphrSerGlyLys	83	
Db	193	GGTGATCTCCATTCCTTTGTACATCCCTCACGCCTGTTCCGATGGGATTTTGGAAAG	252	
Qy	84	GlnAlaCysValPheTrpLeuIleThrAspTyrrLeuLeuCyeThrAlaSerValTyrrAsn	103	
Db	253	GAATCTGTGTATTTTGGCTCAGTCTGACTATCTGTTATGTACAGCATCTGTATATAAC	312	
Qy	104	IleValLeuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTrpTyrrArgAla	123	
Db	313	ATTGTCCTCATCAGCTATGATCGATACCCTGTCAGTCTCAAATGCTGTGTCTTATAGA	372	
Qy	124	GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe	143	
Db	373	CAACATACTGGGGCTTTGAAGATTGTTACTCTGATGGTGGCCGTTTGGGTGCTGGCC	432	
Qy	144	MetThrAndGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys	163	
Db	433	TTAGTGAATGGGCCAAATGATTCTAGTTCTCAGAGTCTTGGAGAGTGAAGGTATG	492	
Qy	164	GluProGlyPheLeuLysLysTrpTyrrPheAlaLeuProThrSerLeuLeuGluPheLeu	183	
Db	493	GAACCTGGATTTTTTTCGGAATGGTACATCCCTTGGCATCACAATCATCTTGGAA	552	
Qy	184	IleProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrTrpSerLeuTrpLysArg	203	

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Db 553 ATCCAGTCATCTTAGTCGCTTATTTCACATGATATATTTATTGGAGCCTGTGGAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
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Db 613 GATCATCTCAGTAGTGCCAAAGCCATCTCGACTGCTGCT--GTCTCTTCCAAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
   :::::::::::::::::::::::::::::
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTTCGCATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
   :::::::::::::::::::::::::::::
Db 730 GTTCTCGATCTCTTTCATTCAGAGACAGACAGAGAGAGAGTAGTCTCATGTTTCTCA 789
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
   :::::::::::::::::::::::::::::
Db 790 AGAACCAAGATGATAGCAATACAAATGCTTCCAAATGGGTCTCTTCTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
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Db 850 TCTGTAGCTCTTCCACCAAGGGAACATGTTGAAGTCTTAGAGCCAGAGATTAGCCAAG 909
Qy 304 SerLeuAlaLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
   :::::::::::::::::::::::::::::
Db 910 TCATCGGCATCTCTTAGGGGTTTGTCTGTGTCTGCTGGCTCCATATCTCTGTTACA 969
Qy 324 VallIeTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTyrHisThrAla 343
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Db 970 ATTGTCCTTCAATTTTATTCCTCAGCAACAGGTCTCTAAATCAGTTGGTATAGAAATTGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
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Db 1030 TTTTGGCTTCAGTGCTCAATTCCTTGTCAATCTCTTTGTATCCCAATTGTCACAAAG 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
   :::::::::::::::::::::::::::::
Db 1090 GCCTTTCAAGAGCTTTCTGAAATATTTGTATAAAGCAACCTCTACCAACAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
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Db 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 13
US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.COM
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Alignment Scores:
Pred. No.: 1,18e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: Gaps: 3

US-10-626-398-10 (1-389) x US-10-417-820A-13 (1-1173)
Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCATTTTATGTCTCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
   :::::::::::::::::::::::::::::
Db 73 GTAGCTTTTGTCTAATAATGCTAGGAAATGCTTTGGTCATTTTGGCTTTTGTGGTGA 132
Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
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Db 133 AACCTTAGACATCGAAGTAGTTATTTTTTTTCTTAACCTTGGCCATCTCTGACTTCT 192
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
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Db 193 GGTGTGATCTCCATTTCTTTGTACATCCTCACACGCTGTTTCGAATGGATTTTGGAA 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
   :::::::::::::::::::::::::::::
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATA 312
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
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Db 313 ATTGTCTCATCAGCTATGATGATACCTGTCAGTCTCAATGCTGTCTTATAGAACT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
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Db 373 CAACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGTGTGGGTGGCTTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
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Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGTGAAGGTAGTGA 492
Qy 164 GluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
   :::::::::::::::::::::::::::::
Db 493 GAACTTGAATTTTTTTCGAATGGTACATCCTTGGCATCACATCATCTTGTGAAATTC 552
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
   :::::::::::::::::::::::::::::
Db 553 ATCCCATCATCTTAGTCGCTTATTTCAACATGATATATTTATGGAGCCTGTGGAAGCG 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
   :::::::::::::::::::::::::::::
Db 613 GATCATCTCAGTAGTGCCAAAGCCATCTCTGAGACTGCT---GTCTCTTCCAAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
   :::::::::::::::::::::::::::::
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTTCTGATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
   :::::::::::::::::::::::::::::
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Db 730 GTTCTGCATCCTTTTCATTTACAGAGACAGAGAGAGTAGTCTCATGTTTCTCTCA 789
 Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
 Db 790 AGAACCAAGATGAATGACCAATCAATTCCTCCAAATGGGTTCCTTCTCCCAATCAGAT 849
 Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
 Db 850 TCTGTAGCTCTTCACCAAGGAGACATGTGAACTGCTTAGAGCCAGAGATTAGCCAG 909
 Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
 Db 910 TCATGGCCATCTCTCTAGGGGTTTTGCTGTGCTGGCTCCATATCTCTGTTCACA 969
 Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
 Db 970 ATTTGCTTTTCATTTTTCCTCAGCAACAGGCTCCTAAATCAGTTTGGTATAGAAATGCA 1029
 Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
 Db 1030 TTTTGGCTTCAGTGGTTCAATCTCTTTGTCAATCTCTTTGTATCCATTTGTGTACAG 1089
 Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
 Db 1090 CGCTTTCAAGGCTTCTTGAATATATTTTGTATAAAAGCAACCTCTACCATCACAA 1149
 Qy 383 HisAsnArgSerIleSerThr 389
 Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 14

US-10-349-253A-1

; Sequence 1, Application US/10349253A
 ; Publication No. US20040043393A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aubart, Kelly
 ; APPLICANT: Bergsma, Derk
 ; APPLICANT: Fitzgerald, Laura
 ; APPLICANT: Graybill, Todd
 ; APPLICANT: Li, Xiatong
 ; APPLICANT: Michalovich, David
 ; APPLICANT: Morrow, Dwight
 ; APPLICANT: Zhu, Yuan
 ; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
 ; FILE REFERENCE: GP70655-2C2
 ; CURRENT APPLICATION NUMBER: US/10/349,253A
 ; CURRENT FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: 09/910,411
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 09/693,761
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/497,790
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/431,898
 ; PRIOR FILING DATE: 1999-11-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-349-253A-1

Alignment Scores:

Pred. No.: 1,188-137 Length: 1173
 Score: 1308.50 Matches: 252
 Percent Similarity: 77.5% Conservative: 48
 Best Local Similarity: 65.1% Mismatches: 84
 Query Match: 64.3% Indels: 3
 DB: 7 Gaps: 3

US-10-626-398-10 (1-389) x US-10-349-253A-1 (1-1173)

Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
 Db 13 AATACCAATCAATTTATCTACTAAGACTCTGTGTACTTTAGCATTTTATGTCTCTTA 72
 Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
 Db 73 GTAGCTTTTGTCTATATGCTAGAAATGCTTTGGTCAATTTTGTAGCTTTTGTGGGACAA 132
 Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAlaPhePheVal 63
 Db 133 AACCTTAGACATCGAAGTAGTTATTTTCTTAACTTTGGCCATCTCTGACTTCTTTGTG 192
 Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
 Db 193 GGTGTGATCTCCATTCCTTTGTACATCCTTCACAGCTGTTCGAATGGGATTTGGAAAG 252
 Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
 Db 253 GAAATCTGTATATTTTGGCTCACTACTGACTATCTGTTATGTATGACGATCTGTATATAAC 312
 Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
 Db 313 ATTGTCTCATCAGCTATGATGATCCTGTGCTCAGTCTCAATATGCTGTGTCTTATGAAC 372
 Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
 Db 373 CAACATCTGGGCTCTTGAAGATTCTTACTCTGATGGTGGCCGTTTGGTGTGCGCTTC 432
 Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
 Db 433 TTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAAGTAGTAATGT 492
 Qy 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
 Db 493 GAACCTGGATTTTTCGGAATGGTACATCTCTTGCATCACATCATCTTCTTGGAAATTCGTG 552
 Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTrpSerLeuTrpLysArg 203
 Db 553 ATCCCAAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATGGAGCTGTGGAGCGT 612
 Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
 Db 613 GATCATCTCAGTAGTGGCCAAAGCCATCTTGGACTGACTGCT---GTCTCTTCCAAATC 669
 Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
 Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTTCAGGAGATCTCTTTCGATCGCAGAA 729
 Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
 Db 730 GTTCTGTCATCTTTCATTTCAGAGAGCAGAGGAGAGAGTAGTCTCATGTTTTCCTCA 789
 Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
 Db 790 AGAACCAAGATGAATGACCAATCAATTCCTCCAAATGGGTTCCTTCTCCCAATCAGAT 849
 Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
 Db 850 TCTGTAGCTCTTCACCAAGGAGACATGTGAACTGCTTAGAGCCAGAGATTAGCCAG 909
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 Db 910 TCATGGCCATCTCTCTAGGGGTTTTGCTGTGCTGGCTCCATATCTCTGTTCACA 969
 Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
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 Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
 Db 1030 TTTTGGCTTCAGTGGTTCAATCTCTTTGTCAATCTCTTTGTATCCATTTGTGTACAG 1089
 Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382

Db 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAACCTCTACCATCAAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 15

US-10-723-955-13
; Sequence 13, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors

FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-955-13

Alignment Scores:
Pred. No.: 1.19e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 7 Gaps: 3

US-10-626-398-10 (1-389) x US-10-723-955-13 (1-1173)

Qy 5 AnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAATCAATTTTACCTACGACCTCGTGTACTTTTACGATTTTATGTCCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGCTATATGCTAGGAATGCTTTGGTCATTTTGTGCTGGACAA 132

Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTTAGACATCGAAGTATATTTTCTTAACCTGGCCATCTCTGACTTTCTTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTATACCTCCACACGCTGTTCGAATGGGATTTTGGAAAG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAAATCTGTGTATTTTGGCTCACTACTACTATCTGTATTGTATACAGCATCTGTATATAAC 312
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
Db 313 ATTGTCTCATTCAGTATGATCGATACCTGTCACTCTCAAAAGTCTGTCTTATAGAACT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATCTGGGTCTTGAAGATTGTACTCTGTATGGTGGCGTTTGGTCTGGCCTTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGAATGGCCCAATGATTCTAGTTTTCAGAGTCTTGGAAAGGATGAAGTAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysLysTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTATACATCTCTCCATCATCATTTCTTGGAAATCTGTG 552
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCACTTAGTCGCTTATTTCAACATGAATATTTATGGAGCTGTGGAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCCAAAGCCATCTCTGAGTCTGCTCTTCTTCCAAATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCAATCGACAAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerSerLeuLeuProSerIle 263
Db 730 GTTCTGCACTCTTTCATTCAGAGAGACAGAGAGAGAGTAGTCTCATGTTTCTCTCA 789
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTCTCTTCTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCACAAAGGGAACATGTTGAACCTGTAGAGCCAGAGATAGCCAAAG 909
Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCATGGGCATCTCTTAGGGGTTTTCGTGTTGCTGGCTCCCATATTTCTCTGTTTCA 969
Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
Db 970 ATTGTCTCTTCAATTTTATTCCTCAGCAACAGGTCTCTAAATCAGTTTGGTATAGAAATGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTATTCATTTGTGTCAAG 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAACCTCTACCATCAAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

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Job time : 3206 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)
2771.638 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036

Sequence: 1 MLANNSTIALTSIKSLTFL.....LKLPRQSTPPHNRISIT 389

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Delop 6.0, Delext 7.0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=2000000000 -HOST=abss04
-USER=US10626398 @CGN_1.1.658 @runat_26042006_101740_18832 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

Published Applications NA.New:*
1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
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10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq5:*
11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
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15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	681.5	33.5	2761	11	US-11-036-196-2003 Sequence 2003, Ap
2	681.5	33.5	2814	14	US-11-136-527-3990 Sequence 3990, Ap

3	620.5	30.5	2824	14	US-11-136-527-127	Sequence 127, App
4	549	27.0	1326	14	US-11-241-956-19	Sequence 19, Appl
5	409.5	20.0	2348	14	US-11-136-527-3691	Sequence 3691, Ap
6	407.5	20.0	4095	14	US-11-136-527-2030	Sequence 2030, Ap
7	404.5	19.9	3578	11	US-11-036-196-1495	Sequence 1495, Ap
8	403.5	19.8	1773	14	US-11-127-877-17	Sequence 17, Appl
9	403.5	19.8	1974	14	US-11-124-368A-14	Sequence 14, Appl
10	402.5	19.8	2733	14	US-11-136-527-2435	Sequence 2435, Ap
11	397	19.5	2699	14	US-11-127-877-5	Sequence 5, Appl
12	392	19.3	2633	14	US-11-136-527-3114	Sequence 3114, Ap
13	389	19.1	3741	14	US-11-136-527-751	Sequence 751, App
14	387	19.0	1862	14	US-11-136-527-2377	Sequence 2377, Ap
15	385.5	18.9	2089	14	US-11-127-877-14	Sequence 14, Appl
16	385.5	18.9	2290	14	US-11-127-877-13	Sequence 13, Appl
17	378	18.6	85980	11	US-11-114-798-46	Sequence 46, Appl
18	378	18.6	197241	11	US-11-114-798-47	Sequence 47, Appl
19	376.5	18.5	2089	14	US-11-128-061-892	Sequence 892, App
20	376.5	18.5	2089	14	US-11-128-049-892	Sequence 892, App
21	373	18.3	1401	14	US-11-127-877-4	Sequence 4, Appl
22	370	18.2	1203	9	US-10-499-210-1	Sequence 1, Appl
23	370	18.2	1860	14	US-11-136-527-2642	Sequence 2642, Ap
24	364	17.9	4061	14	US-11-136-527-2806	Sequence 2806, Ap
25	360	17.7	2483	14	US-11-136-527-2847	Sequence 2847, Ap
26	359.5	17.7	2591	14	US-11-136-527-1944	Sequence 1944, Ap
27	356	17.5	1435	8	US-10-750-185-26145	Sequence 26145, A
28	356	17.5	1435	8	US-10-750-623-26145	Sequence 26145, A
29	356	17.5	2509	14	US-11-136-527-3738	Sequence 3738, Ap
30	348	17.1	1303	14	US-11-128-061-570	Sequence 570, App
31	348	17.1	1303	14	US-11-128-049-570	Sequence 570, App
32	348	17.1	1496	14	US-11-136-527-2608	Sequence 2608, Ap
33	343	16.8	6501	14	US-11-136-527-3427	Sequence 3427, Ap
34	338	16.6	1374	11	US-11-232-805-42	Sequence 42, Appl
35	338	16.6	1443	8	US-10-521-162-39	Sequence 39, Appl
36	338	16.6	1443	8	US-10-521-162-41	Sequence 41, Appl
37	337	16.6	2809	14	US-11-136-527-2036	Sequence 2036, Ap
38	336	16.5	1386	11	US-11-232-805-40	Sequence 40, Appl
39	332.5	16.3	3893	14	US-11-136-527-2295	Sequence 2295, Ap
40	322.5	15.8	1350	11	US-11-232-805-24	Sequence 24, Appl
41	322.5	15.8	1350	11	US-11-232-805-25	Sequence 25, Appl
42	322	15.8	2995	14	US-11-136-527-3388	Sequence 3388, Ap
43	321	15.8	1260	14	US-11-136-527-2149	Sequence 2149, Ap
44	316.5	15.5	1552	14	US-11-136-527-2107	Sequence 2107, Ap
45	314.5	15.4	1344	11	US-11-232-805-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-11-036-196-2003
; Sequence 2003, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgin, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807

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; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 2761
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_053506
US-11-036-196-2003

Alignment Scores:
Pred. No.: 2e-51 Length: 2761
Score: 681.50 Matches: 162
Percent Similarity: 52.7% Conservatives: 65
Best Local Similarity: 37.6% Mismatches: 135
Query Match: 33.5% Indels: 69
DB: 11 Gaps: 13

US-10-626-398-10 (1-389) x US-11-036-196-2003 (1-2761)
QY 3 AlaAsnAsmSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
DB 413 GCGCGGGCTTCGCGGTGCTGCGACCGCTGC-----CTGGCTGGCTCATGGCG 463
QY 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
DB 464 CTGCTCATCGTGCCACACTACTGCGGCAACGCGCTGCTGTCATGTGCGCTTCGCGGGAT 523
QY 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
DB 524 TCGAGCCTCGCGACCCAGAACACTCTTTCTGCTCAACTCGGCATCTCCGACTTCCTC 583
QY 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
DB 584 GTGGTGCTTCGTCATCCCATTCATGCTACCTATGCTGTGTCGACGCGCGCTTGACCTTC 643
QY 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
DB 644 GCGCGGGCTCTGCAAGCTGTGGCTGTGGTAGACTACCTACTGTGTGCTCTCTCGGTC 703
QY 102 TyrAsnIleValIleIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
DB 704 TTCACATCGTACTCATCAGCTATGACCGGATCTCTGTCAGTCACTCGAGCTGTCTCTAC 763
QY 122 ArgAlaGlnHisSerGlyThrTrpTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
DB 764 AGGCCCCAGCGGGGACACAGACGGCGCTTCGGAAGATGGACACTGGGTGGGTCTG 823
QY 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
DB 824 GCCTTCCTGCTGTATGGGCTTGCCTCCTG-----AGTTGGGAGTACCTGTCTGTGGT 874
QY 158 ---AsnSerThrGlu-----CysGluProGlyPheLeuLysLysTrpTyrPheAla 174
DB 875 GCGAGTTCATCCCGAGGGCCACTGCTATGCTGAGTTCCTCTCAACTGGTACTTCTTC 934
QY 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
DB 935 ATCAGGGCTCCACCTCGAGTCTTTCAGCGCCTCTCTCAGCGTGTACTCTTCTCAACCTC 994
QY 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeuSer 211
DB 995 AGCATCTACCTGAACATCCAGAGCGCACCCGCTCTGGCTTGTATGGGGCCGTGAGGCT 1054

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US-10-626-398-10 (1-389) x US-11-136-527-3990 (1-2814)
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QY 23 LeuLeuAlaIleAlaIleMetLeuGlyAenValValIleAlaIleAlaPheIleValAap 42
Db 454 CTGCTCATGTCGCCACAGTACTGGGCAACGGCTGCTCATGCTCGCTCGCTGGCGGAT 513
QY 43 ArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleAlaAapPhePhe 62
Db 514 TCGAGCTCCGGCACCAGACCAACTTCTTCTGCTCAACTCGGCATCTCCGACTTCTCTC 573
QY 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 574 GTGGGTGCTTCTGCTATCCCATGTACGTACCTATGTGTGCTGACCGCGCTTGGACCTTC 633
QY 82 GlyLeuGlnAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 634 GCGCGCGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTACTGTGTGCTCTCTCGGTC 693
QY 102 TyrAenIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaValTyrTyr 121
Db 694 TTCACATGCTACTCATAGTATGACCGATTCCTGTCTGCTCAGTCACTCGAGCTTCTCTAC 753
QY 122 ArgAlaGlnHisSerGlyTyrTrpIleAlaIleThrGlnMetValAlaValTyrIlePhe 141
Db 754 AGGCGCCAGCAGCGGGGACACGAGCGCGCTTCCGAGATGGCACTGGTGTGGGTGCTG 813
QY 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTyrGln-----157
Db 814 GCCTTCTCTGTATGGGCTGCCATCTCTG-----AGTTGGGAGTACCTGTGTGT 864
QY 158 ---AenSerThrThrGlu-----CysGluProGlyPheLeuLeuIleSerTyrPheAla 174
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QY 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
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QY 195 HisIleTyrTrpSerLeuTyrPlysArgGluLeuLeu-----SerArgCysLeuSer 211
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QY 236 -----AlaThrLeuProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 1216 GGAGGTGCTGCTCGCTCGCCACCTCCAGCTTGGCAGCTCTCAAGGGGCACTGAGAGG 1275
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Db 1327 GAGAGCGCATGAGATGTGTCCAGAGC-----ATCACCAGCGC-----1368
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QY 333 AenLeuThrLysSerThrTyrTyrHisThrAlaPheTrpLeuGlnTrpPheAenSerPhe 352
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RESULT 3
US-11-136-527-127
; Sequence 127, Application US/111136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127

Alignment Scores:
Pred. No.: 7,286-46 Length: 2824
Score: 620.50 Matches: 153
Percent Similarity: 49.9% Conservatives: 62
Best Local Similarity: 35.5% Mismatches: 147
Query Match: 30.5% Indels: 69
DB: 14 Gaps: 13

US-10-626-398-10 (1-389) x US-11-136-527-127 (1-2824)
QY 3 AlaAenAenSerThrIleAlaLeuThrSerIleLeuSerLeuThrPheLeuMetSer 22
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QY 23 LeuLeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAap 42
Db 464 CTGCTCATGTCGCCACAGTACTGGGCAACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
QY 43 ArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleAlaAapPhePhe 62
Db 524 TCGAGCCWCSRSRCCSRGMCWCWTKTKCYKWCMAASCTYRSSAKCTCSGACWKSSFC 583
QY 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 584 GTGGGTGCTTCTGCTATCCCATTTGACCTACCTATGTGTGCTGACCGCGCTTGGACCTTC 643
QY 82 GlyLeuGlnAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 644 GCGCGCGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTACTGTGTGCTCTCTCGGTC 703
QY 102 TyrAenIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaValTyrTyr 121
Db 704 TTCACATGCTACTCATAGCTATGACCGATTCCTGTGCTGCTGCTGCTGCTGCTGCTGCT 763
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QY 138 ValTropPheSerPheMetThrAenGlyProMetIleLeuIleSerAspSerTrpGln 157
 Db 574 GTTGGGTGCTGCCCTCTCTAGTAATGGCCCAATGATCTAGTTTTCAGAGTCTTGAAG 633
 QY 158 AenSerThrTrpGluCysGluProGlyPheLeuLysLeuTyrPheAlaLeuProThr 177
 Db 634 GATGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTCCCATCACA 693
 QY 178 SerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyr 197
 Db 694 TCATCTCTGGAAATCGTATGCCAGTCATCTTAGTCGCTTAATTAACAATGAATATTTAT 753
 QY 198 TrpSerLeuTrpLysArgGluLysLeuSerArgCysLeuSerHisPro 213
 Db 754 TGGAGCCTGTGAAGGTGATCATCTCAGG-----CTTGGGCATCCC 795

RESULT 5

US-11-136-527-3691
 ; Sequence 3691, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3691
 ; LENGTH: 2348
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-3691

Alignment Scores:

Pred. No.: 8,88e-27 Length: 2348
 Score: 409.50 Matches: 133
 Percent Similarity: 40.8% Conservative: 83
 Best Local Similarity: 25.1% Mismatches: 143
 Query Match: 20.1% Indels: 171
 Db: 14 Gaps: 16

US-10-626-398-10 (1-389) x US-11-136-527-3691 (1-2348)

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 Db 333 GTCTTCATTCCTCTTAACCGGCTTCCTGGCATTTGGTACCATCATTTGGCAACATCCTT 392
 QY 35 ValIleLeuAlaPheIleValAspArgAenLeuArgHisArgSerAsnTyrPhePheLeu 54
 Db 393 GTCATTTGGGCTTCAAGGTCAACAAACGCTGAGACAGTCAACACTACTTCTCTTA 452
 QY 55 AenLeuAlaIleAlaAspPheValGlyAlaIleAlaIleProLeuTyr-IleProSe 74
 Db 453 AGCCTGGCTGTGCAGACCTGATCATCGGGGTCAITTCATGAACCTGTTCACTACTTAC 512
 QY 74 rSerLeu---ThrTyrTrpTrpSerGlyLysGlnAlaCysValPheTrpLeuIleThrAs 93
 Db 513 ATCATTTGAACCGT-TGGGCACTGGGGAACCTTAGCCTCGGACCTCTCGCTCTCCATTGA 571
 QY 93 pTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspAtqTyrG1 113
 Db 572 CTATGTGGCCAGCAATGCTCTGTCATGATCTGCTGGTCATCAGCTTTCAGAGTACTT 631
 QY 113 nSerValSerAenAlaValTrpTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaTh 133
 Db 632 TTCCATCACTAGGCCACTCACCTACCGAGCCAAAGA-----ACAACAAACGAGCTGG 685
 QY 133 rGlnMetValAlaVal---TrpIlePheSerPheMetThrAenGlyProMetIleLeuI1 152

Db 686 TGTGATGATGCTGGCTTGGGTTCATCTCCTTTGTCTATGGGCTCTCCCATCTTGT 745
 QY 152 eSerAspSerTrpGlnAenSerThrThr-----GluCysGluProGlyPheLe 168
 Db 746 CTGGCAATACTTTGTAGGGAAGAGAACTGTGCCCCCAGGAGAAATGTTTTCAGTTTCT 805
 QY 168 uLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeu 188
 Db 806 GAGTGAAGCCCAACCATCACCTTCGGCAGCGCGATCGCTTTTATACATCGCTGTCA 865
 QY 188 uValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg---GluLysLeuSe 207
 Db 866 CATGACTATT-----TTATACTGGAGGATCTATAGGAACTGAGAGAGGTAC 913
 QY 207 rArgCysLeuSer-----Hi 212
 Db 914 CAAGAGCTGGCTGGCTTACAGGCCTCTGGGACAGAGCGGAGGAGCAAAAACCTTTGTCCA 973
 QY 212 sProValLeuProSerAspSerSerSer----- 222
 Db 974 CCCCAAGGAGCTTCTCGAAGCTGTAGCAGCTATGAACCTGCAACAGAGGTGTGAACG 1033
 QY 222 ----- 222
 Db 1034 ATCATCCAGGAGAAAGTAGGTGCTGCTGTCATCTTCTGGTTCCACCACCAAGAGCTGGAGCC 1093
 QY 223 -----AspHisGlyHisSerCysArg-----GlnAspProAspSe 234
 Db 1094 CAGTCCCGCAGCAGATGGACCAAGACCAAGCAGCAGCAGCAGTTCGGAACAACAGATGC 1153
 QY 234 rArgAlaThrLeuProAlaArgLysGluThrThrAlaSer-----LeuG1 249
 Db 1154 TGCTGCTCCCTG-----GAAAACTCTGCTTCTCCGATGAAGAGACATTGG 1201
 QY 249 ySerAsp-----LysSerArgArgLysSerSerLeuLe 260
 Db 1202 CTCAGACAGCGGCGCATCTATTCAATGTCTCAAGCTTCAGGCTTCAGGCCATAGTCTCATCT 1261
 QY 260 uProSerIleArgAlaTyrLysAenSerAenValIleAlaSerLys----- 275
 Db 1262 CAACCTCTACCAAGCTTACCATCTCTCAGATAACCTCGCAGGTGTCCAACAGGAGACCTGGGAC 1321
 QY 275 ----- 275
 Db 1322 TGTGGATGTGGAGAGAAATGCTCAAGCTTCAGGCCCCAGAGAGCATGGTGGTGA 1381
 QY 276 -----MetG1 277
 Db 1382 CAACGTGCAGAGGATTTCCACAGCTTCCCATCCAGTTAGAGTCTGCTGTGGACACAGG 1441
 QY 277 yPheLeuSerHisSerAspSerLeuAla----- 286
 Db 1442 CAAGACCTCTGCACCAACTCTCTGGCAGACAAGACCAGCGGTACTCTACCTCTGTCTT 1501
 QY 287 -----LeuGlnGlnAr 290
 Db 1502 CAAGGAGCCACGCTGGCTTAAGAGGTTTGTCTCTCAAGACCAGAGTCCAGATCACCAGCG 1561
 QY 290 gGluHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAl 310
 Db 1562 GAAGAGGTGCTGCTCATCAAGGAGAGAAAGCGCCAGAGCGCTCAGTGCCATCTTGT 1621
 QY 310 aAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePhePr 330
 Db 1622 AGCTTTCATCATCAGTGGACCCCTCAACATCATGTGCTCTGGTGAACACCTTC----- 1676
 QY 330 oGluArgAenLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAs 350
 Db 1677 -CGTGACAGCTGCATACCCAAAACCTATTGGAATCTGGGCTACTGGCTGTGTATATCAA 1735
 QY 350 nSerPheValAenProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLe 370
 Db 1736 CAGCACCGTGAACCCCTGTGTCTATGCTCTGTGCAACAAAACATTTCAAGAACCCACCTTCAA 1795

Db 2275 GTCGGTCAATTTTTCACAGCGA 2296

RESULT 7

US-11-036-196-1495

Sequence 1495, Application US/11036196

Publication No. US20060078900A1

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

APPLICANT: Porter, Mark

APPLICANT: Johnson, Kory

APPLICANT: Higgs, Brandon

APPLICANT: Castile, Arthur

APPLICANT: Blaschhoff, Michael

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5089-US

CURRENT APPLICATION NUMBER: US/11/036,196

CURRENT FILING DATE: 2005-01-18

PRIOR APPLICATION NUMBER: US/10/152,319

PRIOR FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: US 60/292,335

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 60/297,523

PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,925

PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,810

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,807

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,808

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/315,047

PRIOR FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: US 60/324,928

PRIOR FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/330,867

PRIOR FILING DATE: 2001-11-01

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2221

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1495

LENGTH: 3578

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURES:

OTHER INFORMATION: Genbank Accession No. NM_012527

US-11-036-196-1495

Alignment Scores:

Pred. No.: 4,358-26 Length: 3578

Score: 404.50 Matches: 130

Percent Similarity: 40.5% Conservative: 84

Best Local Similarity: 24.6% Mismatches: 146

Query Match: 19.9% Indels: 169

DB: 11 Gaps: 15

US-10-626-398-10 (1-389) x US-11-036-196-1495 (1-3578)

QY 15 IleSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaMetLeuGlyAsnValVal 34

Db 242 GTCCTCATGGCTTCTTAACCTGGCTTCCTGGATTTGGTGGACCATCATTTGGCAACATCTT 301

QY 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54

Db 302 GTCATTGTGGCTTCAAGGTCAACAAACAGCTGAAGACAGTCAACACTACTTCTCTTA 361

QY 55 AsnLeuAlaIleAlaAspPheValGlyAlaIleAlaIleProLeuTyr-IleProSe 74

Db 362 AGCTGGGCTGTGCAGACGTGATCATCGGGGTCAITTCATGAACCTGTTCATCTAC 421

QY 74 rSerLeu---ThrTyrThrSerGlyGlnAlaCysValPheThrLeuIleThrAs 93

Db 422 ATCATATGAACCGT-TGGGCACTGGGGAACCTTAGCCTGGGACCTCTGGCTCTCCATTGA 480

QY 93 pTyrIleLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGl 113

Db 481 CTATGTGGCCAGCAATGCTCTGTCAATGAATCTGTGGTCAATCAGCTTTTGACAGGTACTT 540

QY 113 nSerValSerAsnAlaValTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaTh 133

Db 541 TTCATCATAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCT 597

QY 133 rGlnMetValAlaValTyrPhePheSerPheMetThrAsnGlyProMetIleLeuIleSe 153

Db 598 GATGATTGGTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 657

QY 153 rAspSerTrpGlnAsnSerThrThr-----GluCysGluProGlyPheLeuIly 169

Db 658 GCAATACTTTGTAGGGAAGAGAACTGTGCCCCAGGAGAAATGTTTCATTCAGTTTCTGAG 717

QY 169 sLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuVal 189

Db 718 TGAGCCCACTACCTTCGGCAGCGGATCGCTGCTTTTACATGCTGCTGCTGCTGCTGCT 777

QY 189 lAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg---GluLysLeuSerAr 208

Db 778 GACTATT-----TTATACTGGAGGATCTATAAGGAACTGAGAGAGCGTACCAA 825

QY 208 gCysLeuSer-----HisPr 213

Db 826 AGAGCTGGCTGGCTTACAGGCTCTGGGACAGAGCGGAGGAGGAGGAGGAGGAGGAGG 885

QY 213 oValLeuProSerAspSerSerSer----- 222

Db 886 CACAGGCACTTCTCGAGCTGTAGCAGCTATGNACTGCAACAGCAGGCGTGAAGAGTGC 945

QY 222 ----- 222

Db 946 ATCCAGGAGGAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005

QY 223 -----AspHisGlyHisSerCysArg-----GlnAspProAspSerAr 235

Db 1006 TGCCGAGCAGATGGACCAAGACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1065

QY 235 gAlaThrProAlaArgLysGluThrAlaSer-----LeuGlySe 250

Db 1066 TGCTCTCCCTG-----GAAACTGCTCTCCGATGAGAGGAGCATGGCTGCTC 1113

QY 250 rAsp-----LysSerArgArgLysSerSerLeuLeuPr 261

Db 1114 AGAGACCAAGGCTATCTATTCATTTGCTCTCAAGCTTCCAGGCTTCCAGGCTTCCATCTCA 1173

QY 261 oSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLys----- 275

Db 1174 CTCTACCAAGCTACCGTCTCAGATAACCTGCGAGGTGTCCAACGAGGACCTGGGACTGT 1233

QY 275 ----- 275

Db 1234 GGATGTGAGAGAAATGCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 1293

QY 276 -----MetGlyPh 278

Db 1294 CTGTGAGAGGATTTTCCCAAGCTTCCCATCCAGTTAGAGTCTGCGGTGGACACAGGCAA 1353

QY 278 eLeuSerHisSerAspSerLeuAla----- 286

Db 1354 GACCTCTGACACCAACTCTCGGCGAGACAGACCGGCTACTCTACCTCTGCTCTTCAA 1413

QY 287 -----LeuGlnArgGl 291

Db 1414 GGAGGCCAGCTGGCTAAGAGTTTGTCTCAAGACCAAGAGTCAAGTCAAGAGCGGAA 1473

QY 291 uHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAla 311

Db 1474 GAGGATGTGCTCATCAAGAGAGAGAGGCGGCCAGAGCGCTCAGTGCCTCTTCTAGC 1533

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QY 311 aPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPheProG1 331
Db 1534 CTTTCATCATCAGTGGAGCCCTACACATCATGTGCTGGTGAACACCTTCTGTGAC-- 1591
QY 331 uArgAsnLeuThrLysSerTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSe 351
Db 1592 ---AGCTGCATACCCAAACCTATGGATCTGGGCTACTGGCTGTGTATATCAACAG 1647
QY 351 rPheValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLy 371
Db 1648 CACCGTGAACCCGTGTGTATGCTATGCTGTGCAACAAACATTCAGAACCCCTTCAAGAC 1707
QY 371 sIleLeuProVal-----ArgArgG1 378
Db 1708 GCTCTCTTGTGTCAGTGTGCAAAAGGAAGAGCGCAACAGCAGTACCAGCAGAGACA 1767
QY 378 nSerThrProProHisAsnArg 385
Db 1768 GTCGGTCATTTTTCACACCGA 1789
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RESULT 8

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US-11-127-877-17
; Sequence 17, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittael, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Anyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/503,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-17
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Alignment Scores:

Pred. No.:	2,17e-26	Length:	1773
Score:	403.50	Matches:	129
Percent Similarity:	39.2%	Conservative:	79
Best Local Similarity:	24.3%	Mismatches:	152
Query Match:	19.8%	Indels:	171
DB:	14	Gaps:	14

US-10-626-398-10 (1-389) x US-11-127-877-17 (1-1773)

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QY 15 lIeSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaMetLeuGlyAsnValVal 34
Db 205 GTCTTCATCGCTTCTTAACGGGCATCTCTGGCTTGGTGACCATCATCGGCAACATCTG 264
QY 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54
Db 265 GTAATTGTCTATTAAAGTCAACAGCAGCTGAAGACCGGTCAACAACTACTTCTCTTA 324
QY 55 AsnLeuAlaIleAlaAspPhePheValGlyAlaIleAlaIleProLeuTyrIleProSer 74
Db 325 AGCGTGGCTGTGGCGATCTGATTATCGGGGTCACTTCAATGATCTGTTT----- 375
QY 75 SerLeuThrTyr-----TrpThrSerGlyLysGlnAlaCysValPheTrp 89
Db 376 ---ACGACCTACATCATCATGATGATGCGCTTAGGGAACTTGGCCCTGTGACCTCTGG 432
QY 90 LeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyr 109
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Db 433 CTTGCCATTGACTAGTAGCCAGCAATGCGCTCTGTATTGAATCTTCTGGTCATCAGCTTT 492
QY 110 AspArgTyrGlnSerValSerAsnAlaValTrpTrpArgAlaGlnHisSerGlyThrTrp 129
Db 493 GACAGATACCTTTTCCATCAGCAGGCGCTCAGTACCGAGCAACG-----ACAACA 546
QY 130 LysIleAlaThrGlnMetValAlaVal---TrpIlePheSerPheMetThrAsnGlyPro 148
Db 547 AAGAGACCGGTGTGATGATCGGTCTGGCTGGGTGTCATCTCTTTGTCTTGGCTCT 606
QY 149 MetIleLeuIleSerAspSerTrpGlnAsnSerThrThr-----GluCysGlu 164
Db 607 GCCATCTGTCTGCAATACTTTGTTGGAAAGAGAACTGTGCTCCCGGAGAGTGTCTC 666
QY 165 ProGlyPheLeuLysLysTrpTrpPheAlaLeuProThrSerLeuLeuGluPheLeu 184
Db 667 ATTGAGTTCTCTCAGTGAGCCCACTTACTTTTGGCAGCAGCATCGCTGCTTTTATAT 726
QY 185 ProfileLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLys----- 202
Db 727 CCTGTCACTTATGACTATT-----TTATCTGGAGATCTATAAGGAAC 774
QY 202 ----- 202
Db 775 GAAAGCGTACCAAGAGCTTGTGCTGGCTGCAAGCTCTGGGACAGAGGAGAGACAGAA 834
QY 202 ----- 202
Db 835 AACTTTGTCCACCCACGGCAGGTCTTCGAAGCTGCACAGTTACGAACTTCAACAGCAA 894
QY 203 -----ArgGluLysLeuSerArgCys----- 209
Db 895 AGCATGAACCGTTCACAGAGAGAGTATGGCGCTGCCACTTCTGGTTCAACACCAAG 954
QY 210 -----LeuSerHisProValLeuProSerAspSerSerSerSerSerAspHis-GlyHi 226
Db 955 AGCTGGAACCCAGCTCCGAGCAGATGACCAAGACACAGCAGCAGTGCAGTTGGAAC 1014
QY 226 sSerCys-----ArgGlnAspProAspSerArgAlaThrLeu--- 238
Db 1015 AACATGATGTGCTGCTCCCTCGGAGAACTCCGCTCTCCGAGGAGGAGGAGGATGCG 1074
QY 239 -ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSe 258
Db 1075 TCCGAGACGAGAGCATCTACTCCATCGTGTCTCAAGCTTCCGGGTACAGACCATCTCTC 1134
QY 258 rLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPh 278
Db 1135 AACTCCACCAAGTTACCC-TCATCGGACACCTCGAGGTGCTCGAGGAGAGCTGGGAT 1193
QY 278 eLeuSer-----HisSerAspSerIleuAlaLeuGln----- 288
Db 1194 GGTGGACTTGGAGAGGAAAGCCGACAAGCTGCGAGGCCAGAGAGCGTGGACGATGGAGG 1253
QY 288 ----- 288
Db 1254 CAGTTTTTCAAAAGACTTCTCCAGCTTCCCATCCAGTAGAGTCAGCGTGGACACAGC 1313
QY 288 ----- 288
Db 1314 TAAGACTTTCAGCTCAACTCCTCAGTGGGTAAAGAGCGGCCACTTACCTCTGTCTT 1373
QY 289 -----GlnAr 290
Db 1374 CAAGGAAGCACTCTGGCCAGAGGTTTGTCTCTGAAGACCAGAGTCTAGATCACTAAGCG 1433
QY 290 gGluHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAl 310
Db 1434 GAAAGAGATGCTCCCTGGTCAAGGAGAGAAAGCGGCCAGACCTCAGTGGCATCTTGT 1493
QY 310 aAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePhePr 330
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Db 1494 TGCCTTCATCATCTTGGACCCCATACAAACATCATGTTCTGGTGAACACCTTTTGTGA 1553
Qy 330 oGluArgAsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAs 350
Db 1554 C-----AGTCATACCCCAAAACCTTTTGGATCTGGGCTATCGCTGTACATCAA 1607
Qy 350 nSerPheValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLe 370
Db 1608 CAGCACCCTGACCCCGTGTCTATGCTCTGTGCAACAAACATTCAGAACCTTTCAA 1667
Qy 370 uLysLeuProVal-----ArgAr 377
Db 1668 GATGCTGCTGCTGCGCAGTGTGACAAAAAAGAGCGCGCAAGCAGCAGTACCAGCAGAG 1727
Qy 377 gGlnSerThrProProHisAsnArgSer 386
Db 1728 ACAGTCGGTCATTTTTCACAAAGCGCGCA 1755

RESULT 9
US-11-124-368A-14
; Sequence 14, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14

Alignment Scores:
Pred. No.: 2,5e-26 Length: 1374
Score: 403.50 Matches: 129
Percent Similarity: 39.2% Conservative: 79
Best Local Similarity: 24.3% Mismatches: 152
Query Match: 19.8% Indels: 171
DB: 14 Gaps: 14

US-10-626-398-10 (1-389) x US-11-124-368A-14 (1-1974)
Qy 15 IleSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaMetLeuGlyAsnValVal 34
Db 205 GTCTTCATCGCTTCTTAACGGGCACTCTGGCTTGGTGGACCATCATCGGCAACATCTGTG 264
Qy 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54
Db 265 GTAATGTGTCAATTAAGTGTCAACAGAGAGCTGAAGAGCGGTCAACACTACTTCTCTTA 324
Qy 55 AsnLeuAlaIleAlaAspPhePheValGlyAlaIleAlaIleProLeuTyrIleProSer 74
Db 325 AGCCTGGCGCTGTGCGCATCTGATTATTCGGGGTCATTTCAATGAATCTGTTT----- 375
Qy 75 SerLeuThrTyr-----TrpThrSerGlyLysGlnAlaCysValPheTrp 89
Db 376 ---ACGACCTACATCATCATGAATCGATGGCGCTTAGGGAACCTTGGCCTGTGACCTCTGG 432
Qy 90 LeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyr 109
Db 433 CTTCGCAATGACTACGTACCGACGCAATGCCCTCTGTATGAAATCTTCTGTGTCATCAGCTTT 492
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Qy 110 AspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAlaGlnHisSerGlyThrTrp 129
Db 493 GACAGATATCTTTTCCATCAGAGCGCTCACGTCACGAGCCAAACGA-----ACAACA 546
Qy 130 LysIleAlaThrGlnMetValAlaVal---TrpIlePheSerPheMetThrAsnGlyPro 148
Db 547 AAGAGAGCCGGTGTGATCGTCTGGCTTGGTGCATCTCTTGTCTCTTTGGGCTCCT 606
Qy 149 MetIleLeuIleSerAspSerTrpGlnAsnSerThrThr-----GluCysGlu 164
Db 607 GCCATCTTCTTGGCAATATCTTGTGTGAAAGAGAACTGTGCTCCCGGAGAGTGTCTTC 666
Qy 165 ProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIle 184
Db 667 ATTGAGTTCCTCAGTGAGCCCACTTACTTTTGGCAGCAGCATCGCTCTTTTATATG 726
Qy 185 ProfileLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLys----- 202
Db 727 CCTGTCAACCATTTATGACTATT-----TTATACTGGAGGATCTATAAGGAACT 774
Qy 202 ----- 202
Db 775 GAAAGCGTACCAAGAGCTTCTGCTGCTCAAGCCTCTGGCAGCAGAGGAGCAGACAGAA 834
Qy 202 ----- 202
Db 835 AACTTTGTCCACCCACGCGCAGTTCGAAAGCTGCGCAGTTCGAACTTCAACAGCAA 894
Qy 203 -----ArgGluLysLeuSerArgCys----- 209
Db 895 AGCATGAAACGCTCCAACAGAGGAGATGATGCGCGCTGCCACTTCTGGTTCAACACCAAG 954
Qy 210 -----LeuSerHisProValLeuProSerAspSerSerSerSerSerSerHis-GlyHi 226
Db 955 AGCTGGAACCCAGCTCCGAGCAGATGGACCAAGACCAACAGCAGCAGTGCACAGTTGGAAC 1014
Qy 226 sSerCys-----ArgGlnAspProAspSerArgAlaThrLeu-- 238
Db 1015 AACAAATGATGTGCTGCTGCTCCCTGGAGAACTCCGCTCTCCGAGGAGGAGGAGCATGGC 1074
Qy 239 -ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSe 258
Db 1075 TCCGAGACGAGAGCCATCTACTCCATCTGTCTCAAGCTTCCGGGTCAAGCAGCAGCACCCTTC 1134
Qy 258 rLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPh 278
Db 1135 AACTCCACCAAGTTACCC-TCATCGGACAACTCGCAGGTGCTCGAGGAGAGCTGGGAT 1193
Qy 278 eLeuSer-----HisSerAspSerLeuAlaLeuGln----- 288
Db 1194 GGTGGACTTGGAGAGGAAAGCCGACAGCTGCAGGCCCCAGAGAGCGGTGGACATGGAGG 1253
Qy 288 ----- 288
Db 1254 CAGTTTTCCAAAAGCTTCTCCAGCTTCCCATCCAGCTAGAGTCAGCGGTGACACAGC 1313
Qy 288 ----- 288
Db 1314 TAAGACTTCTGACGTCAACTCTCTAGTGGTAAAGACACGGCCACTCTACTCTGTCTT 1373
Qy 289 -----GlnAr 290
Db 1374 CAAGAGACCCACTCTGGCCAAAGAGGTTTGTCTCTGAAGACCAAGAGTCAGATCATCTAAGC 1433
Qy 290 gGluHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAl 310
Db 1434 GAAAGAGATGCTCCCTGGTCAAGAGAGAAAGCGGCCAGACCCCTCAGTGGCATCTTGTCT 1493
Qy 310 aAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePhePr 330
Db 1494 TGCCTTCATCATCTTGGACCCCATACACATCATGTGTTCTGGTGAACACCTTTTGTGA 1553
Qy 330 oGluArgAsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAs 350
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Db 1554 C-----AGTCGATACCAAAACCTTTTGGATCTGGGCTACTGGCTGTGCTACATCAA 1607
Qy 350 nSerPheValaAnProPheLeuTyProLeuCysHisLysArgPheGlnLysAlaPheLe 370
Db 1608 CAGCACCGTGAAACCCCGGTGTCTATGCTCTGTGCAACAAACATTCAGAACCACTTTCAA 1667
Qy 370 uLysIleLeuProVal-----ArgAr 377
Db 1668 GATGCTGCTGCTGTGCCAGTGTGACAAAAAAGAGCGCAAGCAGCAGTACCAGCAGAG 1727
Qy 377 gGlnSerThrProProHisAsnAtqSer 386
Db 1728 ACAGTCGGTCAATTTTTCACAGCGCGCA 1755

RESULT 10
US-11-136-527-2435
; Sequence 2435, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2435
; TYPE: DNA
; LENGTH: 2733
; ORGANISM: Rattus norvegicus
US-11-136-527-2435

Alignment Scores:
Pred. No.: 4,68e-26 Length: 2733
Score: 402.50 Matches: 125
Percent Similarity: 39.4% Conservative: 81
Best Local Similarity: 23.9% Mismatches: 150
Query Match: 19.8% Indels: 167
DB: 14 Gaps: 17

US-10-626-398-10 (1-389) x US-11-136-527-2435 (1-2733)
Qy 4 AsnAsnSerThrIleAlaLeuThrSerIleLys----- 14
Db 992 AATGAAGGACTGTCAACGGCACCCGGTAATCACCAGGCTTTGGAAAGCCATGAGCTG 1051
Qy 15 -----IleSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaIleMetLeuGly 31
Db 1052 TGGGAAGTCAATTACTATTGCTGCTGTGACTCGGGTGTGCTGAGCTGATGACCATTTGGGC 1111
Qy 32 AsnValValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyr 51
Db 1112 AATGCTTGGTCAATGCTCTCTCAAGATCAACAGTCAGCTCAAGACAGTTAACTAACACTAC 1171
Qy 52 PhePheLeuAsnLeuAlaIleAlaAspPhePheValGlyAlaIleAlaIleProLeuTyr 71
Db 1172 TACCTGCTCAGCTTGGCTGTGAGACCTCATCATTTGGCATCTTCTCCATGAACCTCTAC 1231
Qy 72 IleProSerSerLeuThrTyr-----TriThrSerGlyLysGlnAlaCys 86
Db 1232 -----ACGACCTACATCTCTCATGGGAGCGTGGTCTCGGGAGTCTGGCTTGT 1279
Qy 87 ValPheTriPheIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeu 106
Db 1280 GACCTTTGGCTGCACTCGACATATGATGACCAATGCTTCTGTCAATGAACCTTTGGTG 1339
Qy 107 IleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAlaGlnHisSer 126
Db 1340 ATTAGTTTTGAUGCTTACTTTTCCATCACAGACCACTGACGCTACCGGCGCAAGCGT--- 1396
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Qy 127 GlyThrTriPylsIleAlaThrGlnMetValAlaVal---TriPhePheSerPheMetThr 145
Db 1397 ---ACCCCAAAAGAGGGCTGGCATCATGATTGGCTTAGCATGGCTGGCTCTCTTTCATCCTC 1453
Qy 146 AsnGlyProMetIleLeuIleSerAspSerTriPglNAsn----- 158
Db 1454 TGGGGCCGAGCCATCCTC-----TGCTGGCAGTACTTGGTGGGAAGCGGACAGTA 1504
Qy 159 SerThrThrGluCysGluProGlyPheLeuLysLysTriPyrPheAlaLeuProThrSer 178
Db 1505 CCACCTGATGAGTGCAGATCCAGTTCTCTCTCAACCCACCATCATCTTTTGGGACTGCC 1564
Qy 179 LeuLeuGluPheLeuIleProIleLeuValAlaTyrPheSerAlaHisIleTyr--- 197
Db 1565 ATTGCTGCTTCTACATCCCTGTCTCCGTCAATGACCATCTCTACTGCGGATCTACCGG 1624
Qy 197 ----- 197
Db 1625 GAGACAGAGAGCGAACCAAGGACTGSGCTGACCTCCAAGGTTCTGTATTCTGTGGCAGAA 1684
Qy 197 ----- 197
Db 1685 GCCAAGAGAGAGAGAGCCAGCTCAAAGGACCCTGCTCAGATCTTTTATTAGTGCCTAGA 1744
Qy 198 -----TriPheSerLeu----- 200
Db 1745 CCCAGCTGGGCCAGAGAGAAAGGAATCAGGCTCTCTGTCATCTCTCCGTAGAGCACC 1804
Qy 201 -----TriPheArgGlu 204
Db 1805 TCACAACAGAGAAAGACCAACCCAGGCCACTGACCTAAGTGTGCTGAGTGGGAAAAGGCTGAG 1864
Qy 205 LysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerSerSer 223
Db 1865 CAGGTTACTACTGTAGCAGCTACCCC-----TCTTCAGAGGATGAA 1906
Qy 224 -----HisGlyHisSerCysArgGlnAsp 231
Db 1907 GCCAAGCCACCATGACCCCTGCTTTCAATGGTCTACAAGAGTGGCCCAAGAAAGC 1966
Qy 232 ProAspSerArgAlaThrLeuProAlaArgLysGluThr-----ThrAlaSerLeu 248
Db 1967 CCGGGGAAGGAATCCAATACCAAGAGACCAAGGAACAGTTGTGAACACCCGGACTGAA 2026
Qy 249 GlySerAspLysSerArgArgLysSerSerLeuLeuPro---SerIleArgAlaTyrLys 267
Db 2027 AACAGTGACTATGACACTCCCAATATCTTTCTGTCTCCAGCTGTGCTCAGACACTCAAG 2086
Qy 268 AsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp----- 283
Db 2087 AGTCAGAAAGTGTGTGGCTATTAAGTTCCGATTTGGTGGTAAAGCCGATGGGACCCAGGAG 2146
Qy 283 ----- 283
Db 2147 ACTACAATGGTGTGAAAGGTGAAATCATGCCCTGTTCCTTCCAGTGTCCAAAGAC 2206
Qy 284 -----SerLeuAlaLeuGlnArgGluHisIle 293
Db 2207 CCTTCAACAAAGGTCGAGATCCCAACCTCATCAATGACCAACGAAGAGAAATG 2266
Qy 294 GluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAla 313
Db 2267 GTTCTGGTCAAGAGAGGAAGCGGCTCAGACCTTGATGGTCCATCTCTCTGCGCTTCATC 2326
Qy 314 IleCysTriPAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArgAsn 333
Db 2327 ATCAGATGAGCCCTTATAACATC---ATGGTCTGGTGTTCACCTCTCTGTGCAAGTGT 2383
Qy 334 LeuThrLysSerThrTriPyrHisThrAlaPheTriLeuGlnTriPheAsnSerPheVal 353
Db 2384 GTCCCCGTCAACCTCTGG---CACTTGGGTGTACTGGCTGTGTATGTCAACAGCACCATC 2440
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; Sequence 3114, Application US/11136527		; Sequence 3114, Application US/11136527	
; Publication No. US20050287570A1		; Publication No. US20050287570A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Wyeth		; APPLICANT: Wyeth	
; APPLICANT: Mounts, William M		; APPLICANT: Mounts, William M	
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes		; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes	
; FILE REFERENCE: 031896-041000 (AM101086)		; FILE REFERENCE: 031896-041000 (AM101086)	
; CURRENT APPLICATION NUMBER: US/11/136,527		; CURRENT APPLICATION NUMBER: US/11/136,527	
; CURRENT FILING DATE: 2005-05-25		; CURRENT FILING DATE: 2005-05-25	
; PRIOR APPLICATION NUMBER: US 60/574,294		; PRIOR APPLICATION NUMBER: US 60/574,294	
; PRIOR FILING DATE: 2005-05-26		; PRIOR FILING DATE: 2005-05-26	
; NUMBER OF SEQ ID NOS: 362830		; NUMBER OF SEQ ID NOS: 362830	
; SOFTWARE: PatentIn version 3.2		; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 3114		; SEQ ID NO 3114	
; LENGTH: 2633		; LENGTH: 2633	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Rattus norvegicus		; ORGANISM: Rattus norvegicus	
US-11-136-527-3114		US-11-136-527-3114	
Alignment Scores:		Alignment Scores:	
Pred. No.: 4, 02e-25		Pred. No.: 1, 18e-24	
Score: 392.00		Score: 389.00	
Percent Similarity: 44.2%		Percent Similarity: 41.1%	
Best Local Similarity: 27.5%		Best Local Similarity: 23.3%	
Indels: 93		Indels: 118	
Query Match: 14		Query Match: 14	
DB: 13		DB: 14	
US-10-626-398-10 (1-389) x US-11-136-527-3114 (1-2633)		US-11-136-527-751	
QY 23 LeuLeuAlaAlaAlaMetLeuGlyAsnValValValLeuAlaPheLeuValAsp 42		QY 372 eLeuProValArg 376	
Db 246 CTCTGTCTCTAGCTACAGTACAGGCAACCTACTGTGACTCATCTCTCAAGGTCAAC 305		Db 1442 GCTGCTGCTGCCGC 1454	
QY 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaAlaAspPhePhe 62		RESULT 13	
Db 306 ACCGAGCTCAACAGTACAGTACAGTACCTCTCTGCTGAGCTGGCTGCTGCTGCTATC 365		US-11-136-527-751	
QY 63 ValGlyAlaAlaAlaProLeuTyrPheProSerSerLeuThr---TyrTrpThrSer 81		; Sequence 751, Application US/11136527	
Db 366 ATGGCACTTCTCCATGAACTCTATACACGTAACCTGCTCATGGGCCACTGGGCTCTG 425		; Publication No. US20050287570A1	
QY 82 GlyLysGlnAlaCysValPheTrpLeuLeuThrAspTyrLeuLeuCysThrAlaSerVal 101		; GENERAL INFORMATION:	
Db 426 GGCACACTGCTGTGACCTCTGCTGGTGGCTGGCTGGCTATGTGGCCAGCAACCCCTGTC 485		; APPLICANT: Wyeth	
QY 102 TyrAsnLeuValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121		; APPLICANT: Mounts, William M	
Db 486 ATGAATCTTCTGCTCATCAGCTTTGACCGTTACTCTCGGTGACCGGACCCCTGAGCTAC 545		; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes	
QY 122 ArgAlaGlnHisSerGlyThrTrpLysAlaAlaThrGlnMetValAlaVal---TrpIle 140		; FILE REFERENCE: 031896-041000 (AM101086)	
Db 546 CGAGCCCAAGCGC-----ACTCCCGAAGGGCAGCTCTGATGATTGGCTAGCATGGCTG 599		; CURRENT APPLICATION NUMBER: US/11/136,527	
QY 141 PheSerPheMetThrAsnGlyProMetIleLeuLeuSerAspSerTrpGlnAsnSerThr 160		; CURRENT FILING DATE: 2005-05-25	
Db 600 GTTTCCTCTGTTCTCTGCGGCCCGCAGCCATCTCTTC-----TGGCAATACCTAGTT 650		; PRIOR APPLICATION NUMBER: US 60/574,294	
QY 161 ThrGlu-----CysGluProGlyPheLeuLysLysTrpTyrPhe 173		; PRIOR FILING DATE: 2005-05-26	
Db 651 GGGGAGCGGACAGTGTGCTGGCGCAGTGTATCATCCAGTTCTCTCCCAACCCATCATC 710		; NUMBER OF SEQ ID NOS: 362830	
QY 174 AlaLeuProThrSerLeuLeuGluPheLeuLeuProIleLeuLeuValAlaTyrPheSer 193		; SOFTWARE: PatentIn version 3.2	
Db 711 ACTTTTGGCACGCCATGGCGGCTTCTACCTCTCCCTGTGTCAGGTCTCATG----- 758		; SEQ ID NO 751	
QY 194 AlaHisIleTyrTrpSerLeuTrpLys-ArgGluLysLeuSer----- 207		; LENGTH: 3741	
Db 759 TGTACACTGTACTTGGCGCATCTACCGGGGACAGAAACCGAGCCCGGAGCTGGCGCGC 818		; TYPE: DNA	
QY 208 ----ArgCysLeuSerHisProValLeuProSerAspSerSerSerAspHisGlyHil 226		; ORGANISM: Rattus norvegicus	
Db 819 CTGAGGGGCTCTGAGACACAGGCAAGGTGGTGGCAGCAGCAGCTCAGAGAGGTCA 878		US-11-136-527-751	
Alignment Scores:		Alignment Scores:	
Pred. No.: 1, 18e-24		Pred. No.: 3741	
Score: 389.00		Matches: 113	
Percent Similarity: 41.1%		Conservative: 86	
Best Local Similarity: 23.3%		Mismatches: 167	
Indels: 118		Indels: 118	
Query Match: 14		Gaps: 14	
DB: 14			

QY 226 sSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGluThrThrAl 246		QY 226 sSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGluThrThrAl 246	
Db 879 CAGC-----CAGGGGCTGAAGGCTCACCCGAGTCGCTCCAGGCGCGCTGC 923		Db 879 CAGC-----CAGGGGCTGAAGGCTCACCCGAGTCGCTCCAGGCGCGCTGC 923	
QY 246 a-----SerLeuGlySerAspLysSerAr 254		QY 246 a-----SerLeuGlySerAspLysSerAr 254	
Db 924 TGGCGCTGTTGCCGGGCACCCAGGCTCCTCAGGCTTACAGCTGGAGAGGAAGAAGAG 983		Db 924 TGGCGCTGTTGCCGGGCACCCAGGCTCCTCAGGCTTACAGCTGGAGAGGAAGAAGAG 983	
QY 254 Arg-----LysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSe 269		QY 254 Arg-----LysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSe 269	
Db 984 GAGGATGAAGGCTCATGAGTCCCTCATCTCCGAGAGTGGAGGCTGGCTGCAGAA 1043		Db 984 GAGGATGAAGGCTCATGAGTCCCTCATCTCCGAGAGTGGAGGCTGGCTGCAGAA 1043	
QY 269 rAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAla 286		QY 269 rAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAla 286	
Db 1044 GTG-GTGATCAAGATGCCATG-----GTAGATTCTGAAGCACAGGCACC 1087		Db 1044 GTG-GTGATCAAGATGCCATG-----GTAGATTCTGAAGCACAGGCACC 1087	
QY 286 ----- 286		QY 286 ----- 286	
Db 1088 CACCAAGCAGCCTCCCAAAAGCTCCCAANTACAGTCAAGAGGCCACCAAGAAGGCCG 1147		Db 1088 CACCAAGCAGCCTCCCAAAAGCTCCCAANTACAGTCAAGAGGCCACCAAGAAGGCCG 1147	
QY 287 -----LeuGlnGlnArgGluHi 292		QY 287 -----LeuGlnGlnArgGluHi 292	
Db 1148 AGACCGAGGGCGCAAGGGCCAAAACCCCGAGGAGGAAGAACAGCTGGCCAAAGAGAAGAC 1207		Db 1148 AGACCGAGGGCGCAAGGGCCAAAACCCCGAGGAGGAAGAACAGCTGGCCAAAGAGAAGAC 1207	
QY 292 sIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPh 312		QY 292 sIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPh 312	
Db 1208 CTTCTCTGCTCAAGAGAGGAAGAGGAGCTCGGAGCTCGGAGCTCGGAGCTCGGAGCTT 1267		Db 1208 CTTCTCTGCTCAAGAGAGGAAGAGGAGCTCGGAGCTCGGAGCTCGGAGCTCGGAGCTT 1267	
QY 312 eAlaIleCysTrpAlaProTyrSerLeuThrValIleTyrSerPhePheProGluAr 332		QY 312 eAlaIleCysTrpAlaProTyrSerLeuThrValIleTyrSerPhePheProGluAr 332	
Db 1268 CATCTCACCTGAGCACCACCATATAACATCATGGTGTGTGTATCTACTTCTGC-----AA 1321		Db 1268 CATCTCACCTGAGCACCACCATATAACATCATGGTGTGTGTATCTACTTCTGC-----AA 1321	
QY 332 gAsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPh 352		QY 332 gAsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPh 352	
Db 1322 GGACTGTGTTCTCTGAAACCCCTGTGGGAGCTGGGCTACTGGCTATGCTACGTCAACAGCAC 1381		Db 1322 GGACTGTGTTCTCTGAAACCCCTGTGGGAGCTGGGCTACTGGCTATGCTACGTCAACAGCAC 1381	
QY 352 eValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIil 372		QY 352 eValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIil 372	
Db 1382 TGTCAACCCCATGTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1441		Db 1382 TGTCAACCCCATGTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1441	

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US-10-626-398-10 (1-389) x US-11-136-527-751 (1-3741)
QY      1 MetLeuAlaAsnSerThrIleAlaLeuThrSerIleIysIleSerLeuThrPheLeu 20
Db      1030 ATGTGTAGGGGAACAGGACAGCATGGCCACCCCTCAGCTGCTGCCCTGGTGGTGTG 1089
QY      21 MetSerLeuAlaIleAlaIleMetLeuGlyAsnValValIleValIleLeuAlaPheIle 40
Db      1090 CTWAGTAGTATCTCCCTGTCACAGTGGGCGCTCAACCTGCTGCTGTGTAYGCGWTGCR 1149
QY      41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaPhe 60
Db      1150 AGTGARCGAAGCTACACACCGTGGCAACCTRTACATTGTGAGCTGTGCTGTRGCAGAC 1209
QY      61 PhePheValGlyAlaIleAlaIlePro-----LeuTyrIleProSerSerLeuThr 77
Db      1210 CTGATTGAGGGCGAGTGTCAATGCCCATGACATCTCTATCTY-----ATCATGAGCY 1263
QY      78 TyrTrpThrSerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCys 97
Db      1264 AAGTGGTCTCTGCGCGCCCTCTGCTCTTTTGGCTTCTATGATTAATGTCGCCAGC 1323
QY      98 ThrAlaSerValTyrAsnIleValIleSerTyrAspArgTyrGlnSerValSerAsn 117
Db      1324 ACRGATCATCTTTAGTGTCTTCACTCTGCTGTGATGCTGCTACGCTCTGCTCCAGCAA 1383
QY      118 AlaValTrpTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrClnMetValAla 137
Db      1384 CCCCTCCGGTACCTGAGGTAYCGAACCAGACCCGKGTTCMGCTACC---ATCTGGGG 1440
QY      138 ValTrpIlePheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln 157
Db      1441 GCCTGGTCTTCTCTCTGCTGGGTATACCTATCTT-----GGCTGGCAT 1488
QY      158 Asn-----SerThrThrGluCysGluProGlyPheLeuLys 169
Db      1489 CACTTCAYGCCCCYRCCCGCCAGAGCTTCGGGAAGAAVAGTGTGAGACAGATTTCTACAAT 1548
QY      170 LysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuVal 189
Db      1549 GTCACTTGGTTCAAGATCATGACGTCATATATATATATATATATATATATATATATAT 1608
QY      190 AlaTyrPheSerAlaHisIleTyrTrpSerLeuTyrLysArgGluLysLeuSerArgCys 209
Db      1609 CTGTGCTTCTATGTGAAGATCTACAGGCTGTG---CGCGACACTGTGACGACCGCCAG 1665
QY      210 LeuSerHisProValLeuProSerAspSerSer-----SerSerAspHisGly 225
Db      1666 CTCACCAACGGGTCCCTCCCTWCCTTTTVAAGAAATCAAGCTGAGCTCRGASATRCCAAR 1725
QY      226 HisSerCysArg-----Gln 230
Db      1726 GARGGTGCCAAGAAACCTCGGARAGAGTCTCCCTGGGGGGTYCWAAGARAGGCGCRTCAAGA 1785
QY      231 AspPro-----AspSerArgAlaThrLeuProAlaArgLysGluThrAla 246
Db      1786 GACCCYASTGKAGWCTGATCAGAAGTCAACATCTGAAGACCCCAAGRTGACCTCTCCR 1845
QY      247 SerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIleArg----- 264
Db      1846 ACTGTCCTTCAGGCAAGAGGGGAAGGGAACAGTACACAGYCCCTGTTTCGCTTYGAC 1905
QY      265 -----AlaTyrLysAsnSerAsn 270
Db      1906 RTCATGCAGAMACAGYCTGTGTCGTCAGGGAGATGYCAGGGGCTCAAGGCCAATGAYCAG 1965
QY      271 VallIleAlaSer-----LysMetGlyPhe 278
Db      1966 RCCTTGAGCCAGCCCAAAATGATGAGCAGAGCCTGARTACTTGYCGCGGATCAGTGAG 2025
QY      279 LeuSerHisSerAspSerLeuAlaLeuGlnGln----- 289
Db      2026 ACATCAGAGGAYCAGACCTTGTGTGATCTACAGTCTCTCTCCCGACACACAGACTCAGAC 2085
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US-11-136-527-2377
; Sequence 2377, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent version 3.2
; SEQ ID NO 2377
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2377

Alignment Scores:
Pred. No.: 7,33e-25 Length: 1862
Score: 387.00 Matches: 115
Percent Similarity: 44.4% Conservative: 63
Best Local Similarity: 28.7% Mismatches: 139
Query Match: 19.0% Indels: 84
DB: 14 Gaps: 16

US-10-626-398-10 (1-389) x US-11-136-527-2377 (1-1862)
QY      4 AsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db      69 TCCAACTGCACCCACCCACCCAGCTCCGCTGAACATTTCTAAGGCCATTTCTGCTGGGGTG 128
QY      24 -----LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPhe 39
Db      129 ATCTTGGGGGCGCTCATCATTTTCGGAGTYCTGGGAACATTTTAGTGATCTCTCAGTG 188
QY      40 IleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAla 59
Db      189 GCCTGTCTATCGGCATCTGCACTCCGCTGACTCACTACTACTATTGTGTCRCYTGCTGGCA 248
QY      60 AspPhePheValGlyAlaIleAlaIleProLeu-----TyrIleProSerSerLeuThrTyr 78
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Db	249	 GACCTCCTCCTCACCTCCACTGCTGCTGCCTTCTCTGCCACTCTTTGAGATCTTGGGCTAC	308
Qy	79	 TTPThrSerGlyLysGlnAlaCysValPheTrpLeuLeuThrAspTyrLeuLeuLeuCysThr	98
Db	309	 TGGGCCTTTGGCAGGGTGTTCTCAATATCTGGCGCGCTGAGCGTCTTATGCTGCACA	368
Qy	99	 AlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAla	118
Db	369	 GCCTCCATCATGGGCTCTGCATCATCTCCATGACCGGATACATTGGTGTGAGCTACCGG	428
Qy	119	 ValTyrPyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGln	134
Db	429	 CTGCGCTATCCACC-----ATTGTCAACCAGAGGAGGGCGGTC	467
Qy	135	 -----MetValAlaValTrrIlePheSerPheMetThrAsn-----GlyProMetIleLeu	151
Db	468	 AGGGCTCTGTCTGCGCTGGGCTTCTTGGTCATCTCTCCATCGGACCCCTGTTC	524
Qy	152	 IleSerAspSerTrpGlnAsnSerThrThrGlu-----Cys-----	163
Db	525	 -----CGCTGGAGGACCGGCTCCAGAGGATGAGACCATCTGCCAGATCAATGAG	575
Qy	164	 GluProGlyPheLeuLysLysTyrTyrPheAlaLeuProThrSerIleuLeuGluPheLeu	183
Db	576	 GAGCGGGCTACGTG-----CTGTCTCAGCGCTGGGCTCTTCTTCTAC	617
Qy	184	 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrrLysAsq	203
Db	618	 GTGCCACTTGCCCATCAVCTGGTTATGTACTGTGCGAGTCTTAC-----GTAGTAGCCAGAGA	674
Qy	204	 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp	223
Db	675	 GAA-----AGCCGGGGCCTCAAGTCGGC-----CTCAAGCGGCAAGTCAGACTCAGAG	725
Qy	224	 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu	243
Db	726	 -----CAAGTGACGCTCCGCACTCCACCGTAAA	752
Qy	244	 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle	263
Db	753	 AATGTCCTTGCAGAAGCGCGGAGTCAGAGTGCCAGAAGTAAGACTACTCTCTCAGTG	812
Qy	264	 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283
Db	813	 AGGCTGCTCAAGTTTTCT-----	830
Qy	284	 SerLeuAlaLeuGlnGlnArgGluHisIleLeuPheArgAlaArgLysLeuAlaLys	303
Db	831	 -----CGAGAGAAGAAGCTGCCAAG	851
Qy	304	 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr	323
Db	852	 ACGCTTGGGCATCTGCTGGGGTTGCTCTGCTGCTGGCTGGCGTCTCTCCCTAGTGATG	911
Qy	324	 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrrTyrHisThrAla	343
Db	912	 CCCATTGGGTCTTCTTCCCCGGATTTCAG-----CCTTCGGNAACCGTTTTTAAATAGTA	968
Qy	344	 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys	363
Db	969	 TTTTGGCTCGGGTATCTAAATAGTTGCATCAACCTCATATACCCATGTCTCCAGCCAG	1028
Qy	364	 ArgPheGlnLysAlaPheLeuLysIleLeuProVal-----ArgArgGlnSer	379
Db	1029	 GAGTTTCAAGAAAGCCTTTTTCAGAAATCTCTGCGAATCCAGTGTCTTCGACGAAGGCACTCT	1088
Qy	380	 Thr 380	
Db	1089	 TCC 1091	

RESULT 15
US-11-127-877-14

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; Sequence 14, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Pascal G.
; APPLICANT: Merchiers, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27-800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 14
; LENGTH: 2089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-14

Alignment Scores:
Pred. No.:      1.16e-24          Length:      2089
Score:           385.50          Matches:     115
Percent Similarity: 44.8%       Mismatches:   66
Best Local Similarity: 28.5%    Indels:       83
Query Match:      18.9%        Gaps:         16
DB:               14

US-10-626-398-10 (1-389) x US-11-127-877-14 (1-2089)

Qy      3 AlaAsnAnSerThrIleAlaLeuThrSerIleIlystleSerLeuThrPheLeuMetSer 22
Db      467 AGCTTCAACTGCACCCACCAGCGGCGCACCGGTGAACATTTCACAGGCCATTTCTCTGGG 526
Qy      23 Leu-----LeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAla 38
Db      527 GTGATCTTGGGGGCGCTCATCTTTTCGGGGTGCTGGGTAACATCTTAGTGATCCTCTCC 586
Qy      39 PheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIle 58
Db      587 GTAGCCTGTCCACCGACACCTGCACCTCAGTCACGCACCTACTACATCGCTCAACTCGCGGTG 646
Qy      59 AlaaspPheValGlyAlaIleAlaIleProLeu--TyrIleProSerSerLeuThr 77
Db      647 GCCGACCTCTCGTCTCACCTCCACCGGTGTGCCCTTCTCCGCCATCTTCGAGGTCTTAGGC 706
Qy      78 TyrTrpThrSergLyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCys 97
Db      707 TACTGGGCTTCGGAGGGTCTTCTGNAACATCTGGGCGGCAGTGGATGTGTGTGCTGC 766
Qy      98 ThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 117
Db      767 ACCGGTCCATCATGGGCTCTGCATCATCTCCATCGACCGCTACATCGGGGTGAGCTAC 826
Qy      118 AlaValTrpTyrArgAlaGlnHisSerGlyThrTrpIlyslIleAlaThrGln----- 134
Db      827 CCGCTGCGCTACCCAACC-----ATCGTCACCCAGAGGAGGGGT 865
Qy      135 -----MetValAlaValTrpIlePheSerPheMetThrAsn--GlyProMetIle 150
Db      866 CTCATGGCTCTGCTGTGGTCTGGGCACCTCTCCCTGGTGCATATCCATTGGACCCCTGTC 925
Qy      151 LeuIleSerAspSerTyrGlnAsnSerThrThrGlu-----Cys----- 163
Db      926 -----GGCTGGAGGCGAGCGGCCGCCCGAGGACGAGACCATCTGCCAGATCAAC 973
Qy      164 ---GluProGlyPheLeuIlysIysTrpTyrPheAlaLeuProThrSerLeuLeuGluPhe 182
Db      974 GAGGAGCGGGTACGTG-----CTCTTCTCAGCGCTGGGCTCTTC 101
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